



AVIRIS-NG and field data to explore functional traits

Phil Townsend



Imaging Spectroscopy for Plant Traits

Phil Townsend

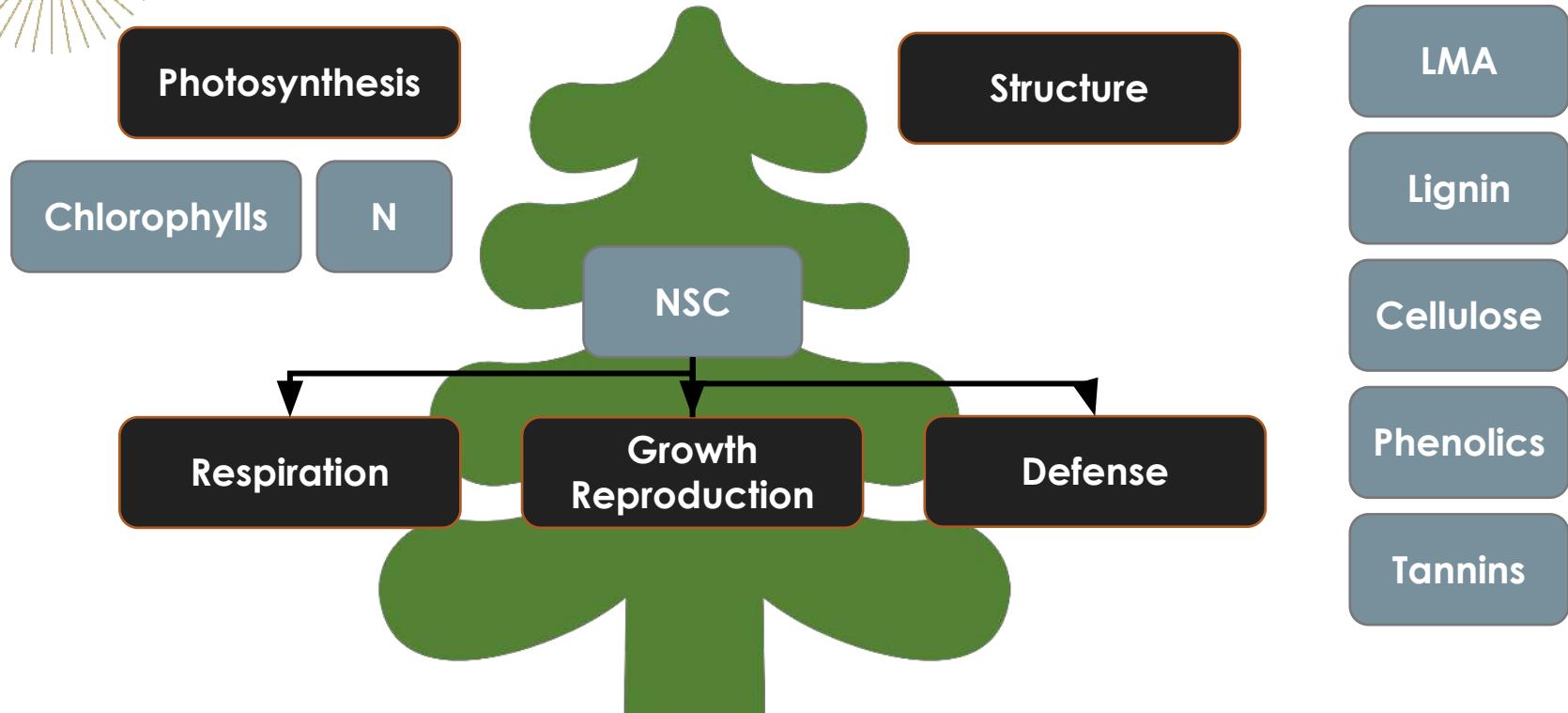
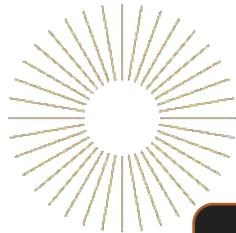
Acknowledgments: Adam Chlus, Phuong Dao, Henry Frye, Kyle Kovach, Shawn Serbin, Aditya Singh, Zhihui Wang, Sarah Wegmueller, Ting Zheng



Includes both:

**AVIRIS-NG and field data to explore
functional traits**





Sample Collection

- Sample sunlit foliage (top of canopy)

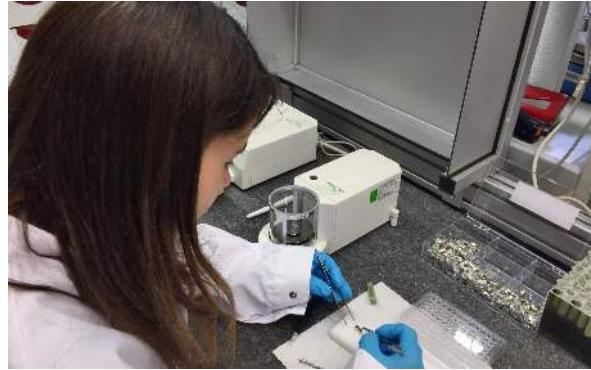


Sample Collection

Field assays



Lab assays



Fresh spectra

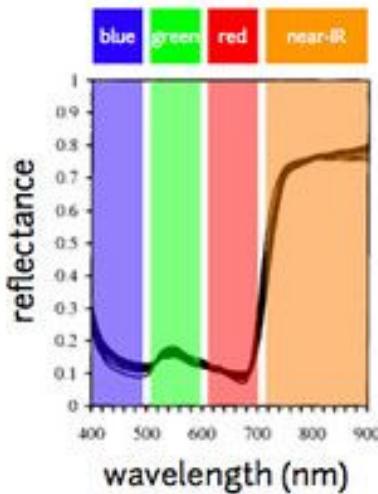


Dry spectra

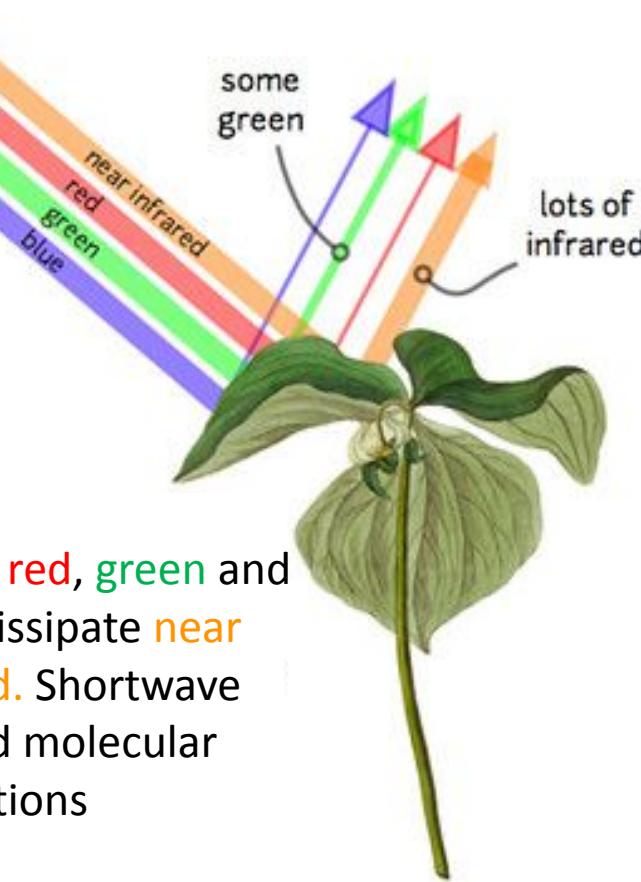




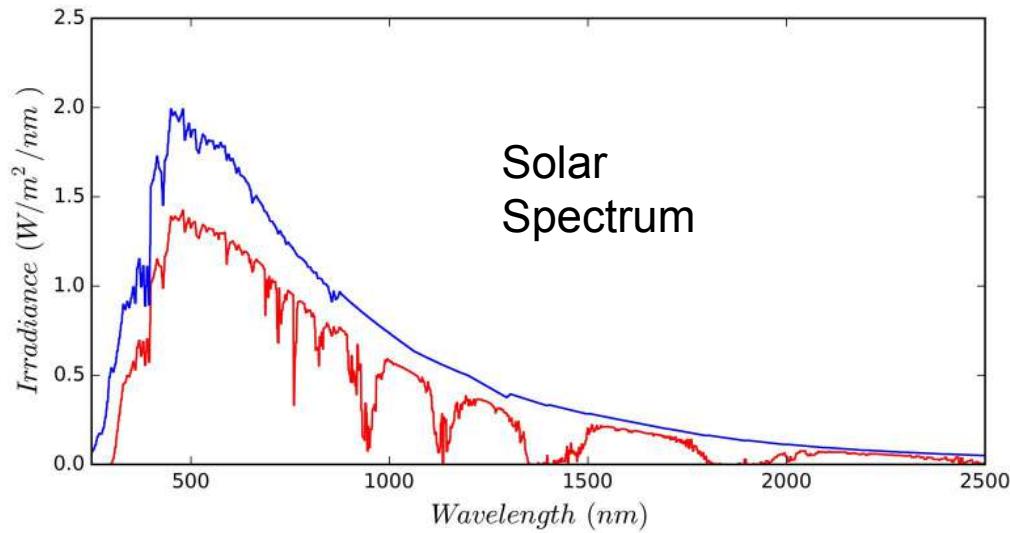
Why do plants reflect lots of infrared light?



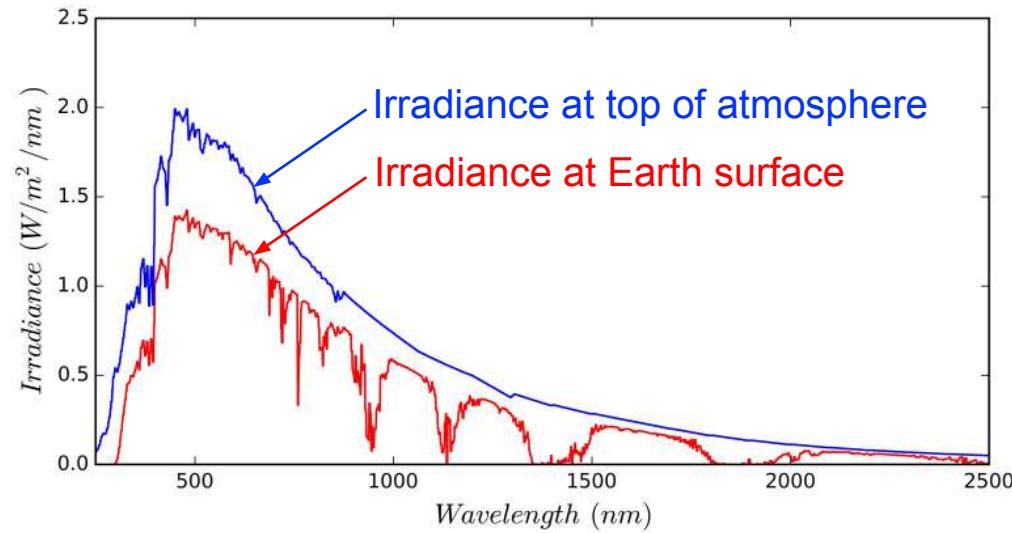
Absorb **red**, **green** and **blue**. Dissipate **near infrared**. Shortwave infrared molecular interactions



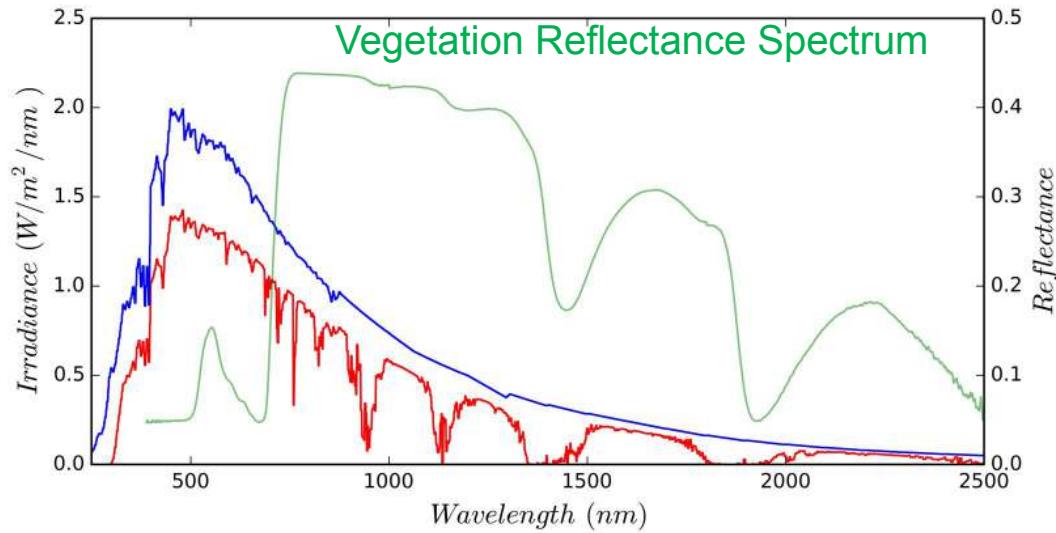
Photosynthesis and Radiation



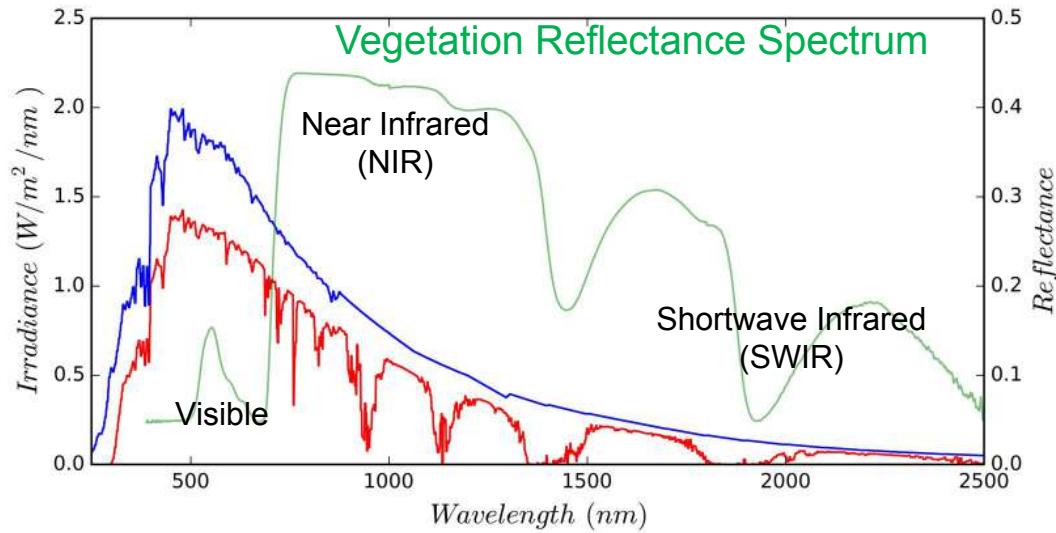
Photosynthesis and Radiation



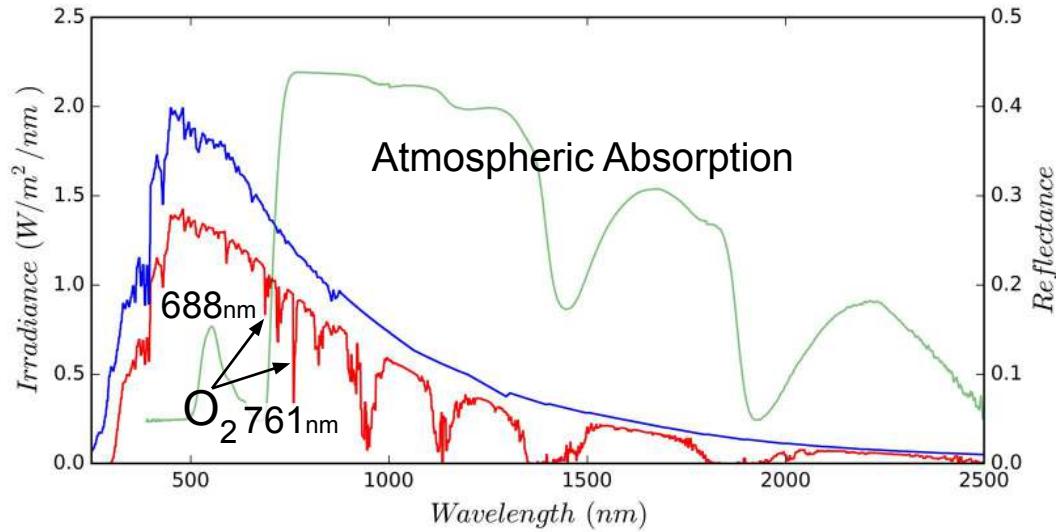
Photosynthesis and Radiation



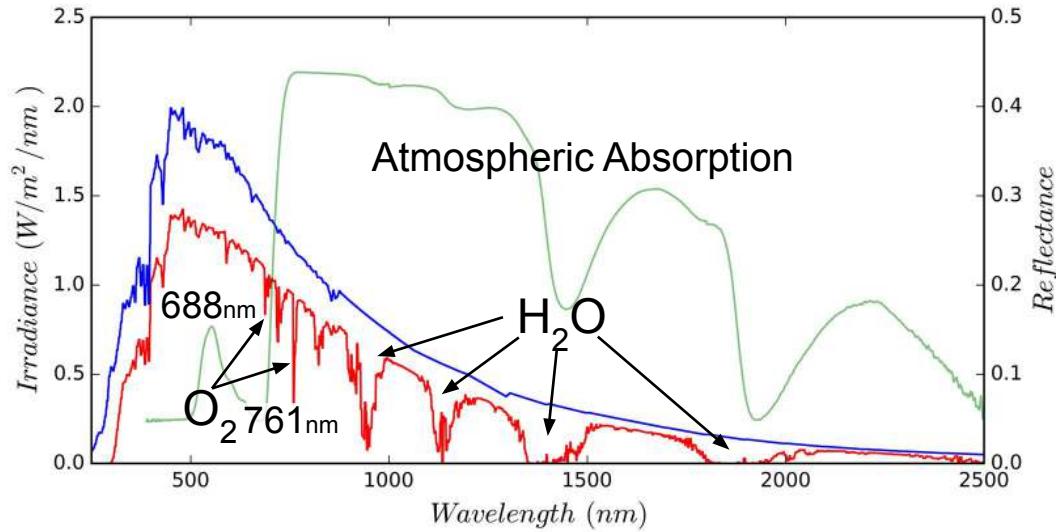
Photosynthesis and Radiation



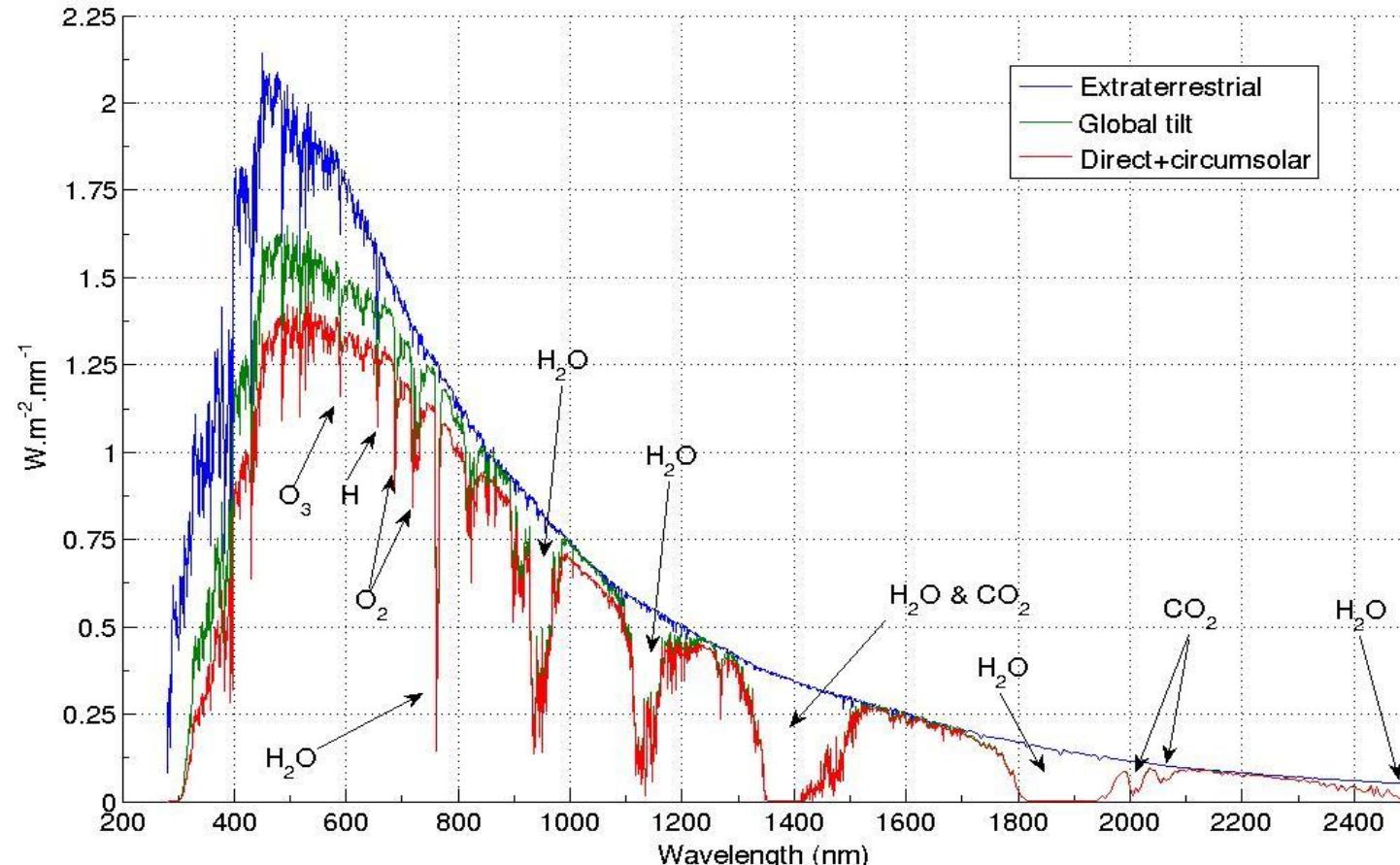
Photosynthesis and Radiation



Photosynthesis and Radiation



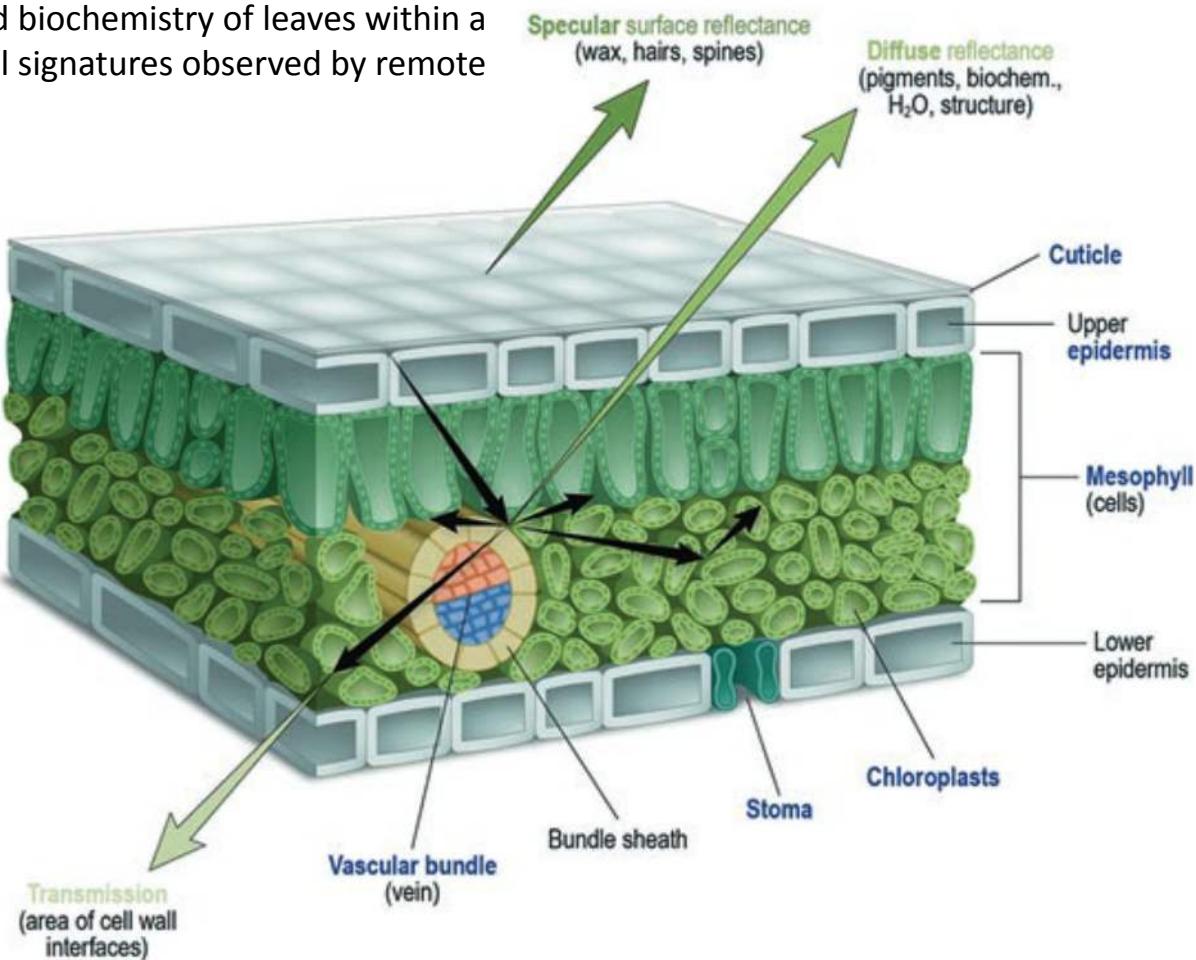
The sun is our light source.....

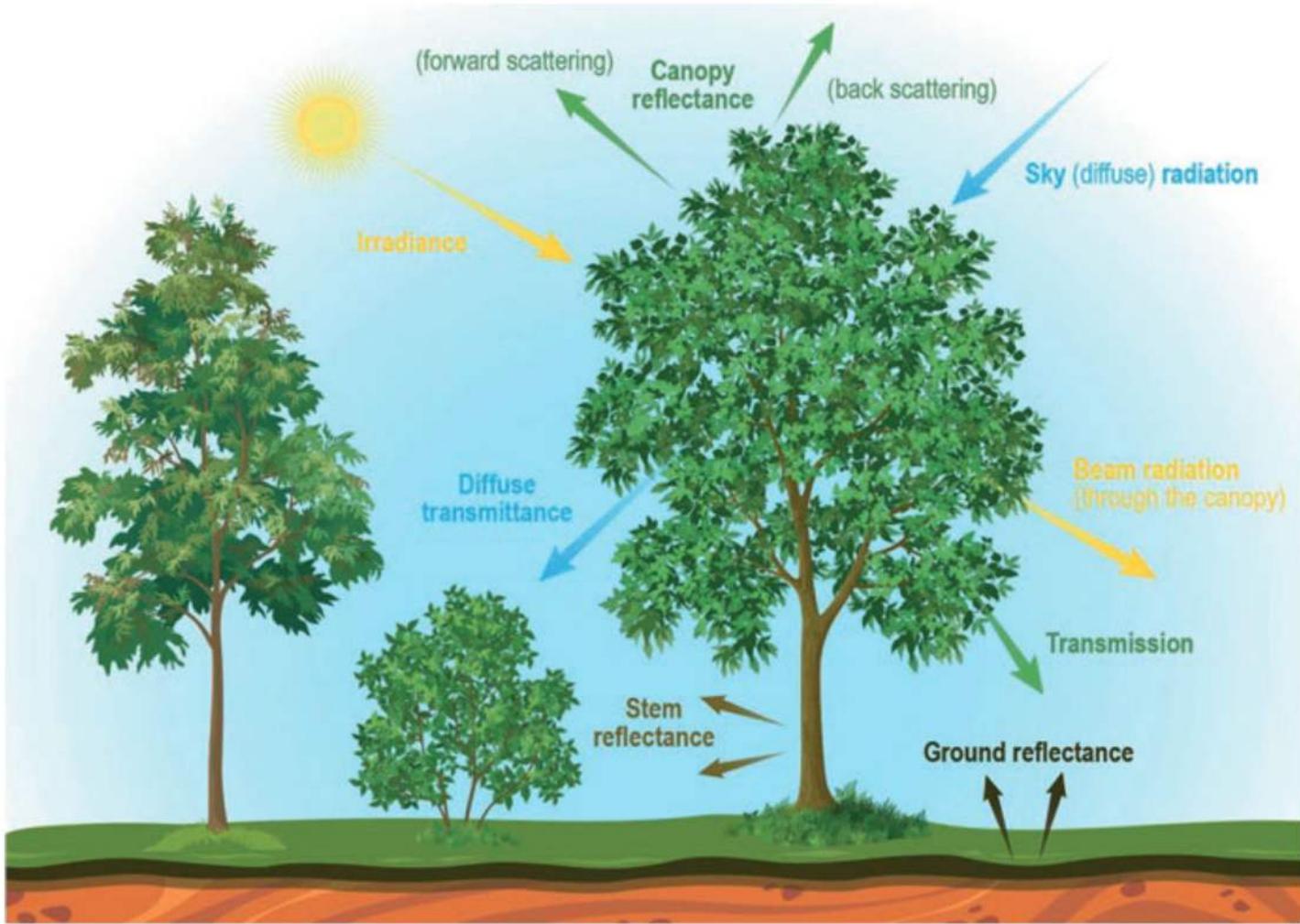


The internal structure and biochemistry of leaves within a canopy control the optical signatures observed by remote sensing.

More complex leaves:

- More internal scattering
- Lower transmission
- More diffuse scattering





Plant Traits from Imagery – An Analogy



4-band MULTISPECTRAL
Red, Green, Blue, and
Near Infrared (NIR)



8-12 band MULTISPECTRAL
Red, Green, Blue, NIR
+
Short wave infrared (SWIR),
Red Edge, others

Most airborne imagery



Hundreds of bands: HYPERSPECTRAL
Able to distinguish many more
colors and tree traits

AVIRIS-NG, EMIT

Most satellites

Reflectance Spectroscopy

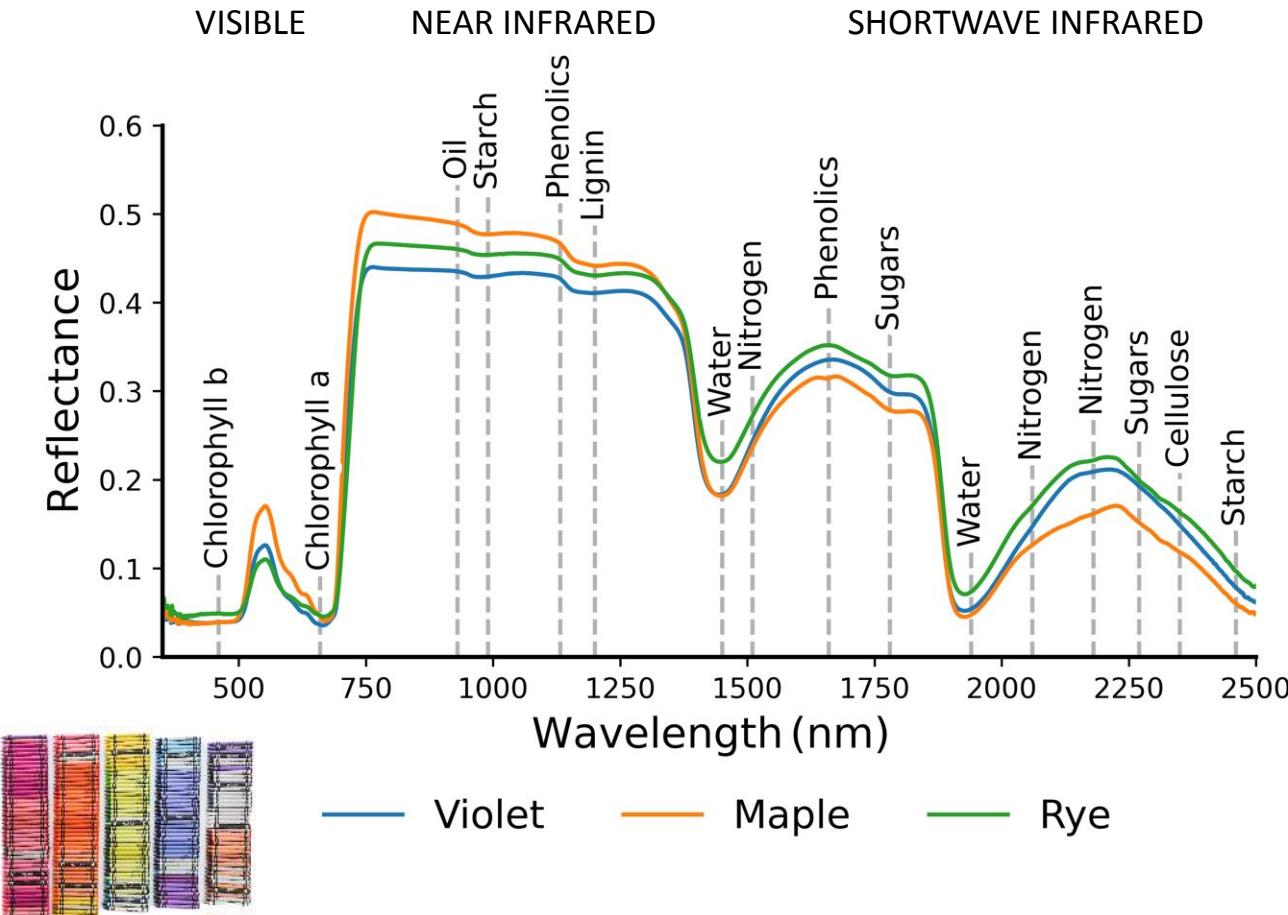


Figure: Adam Chlubas

Reflectance Spectroscopy

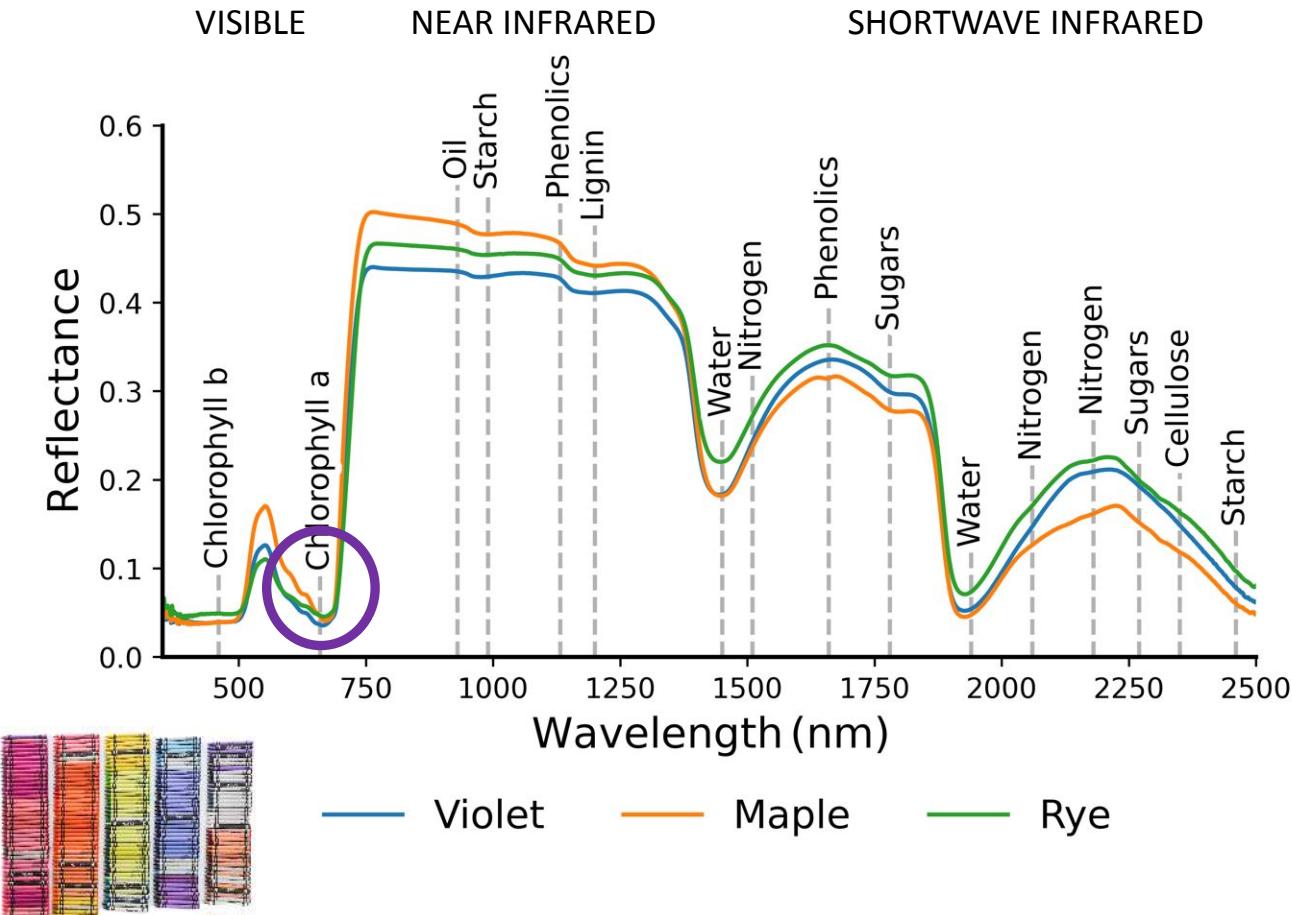


Figure: Adam Chlubas

Reflectance Spectroscopy

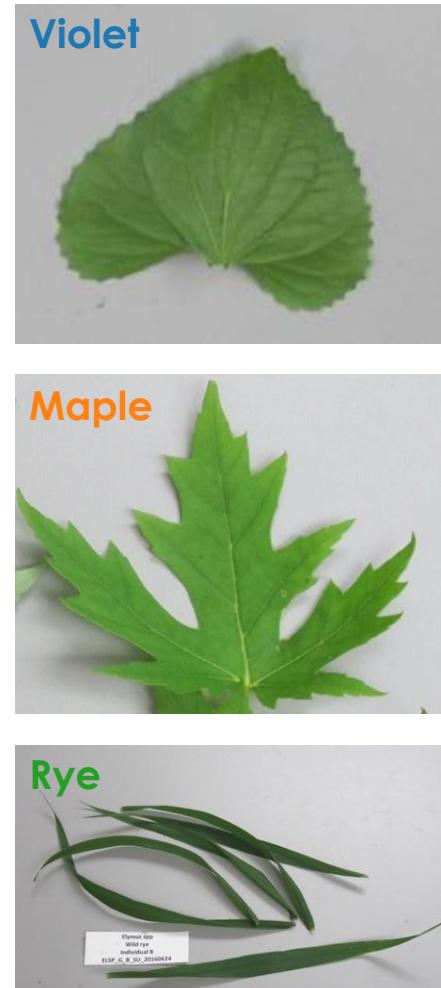
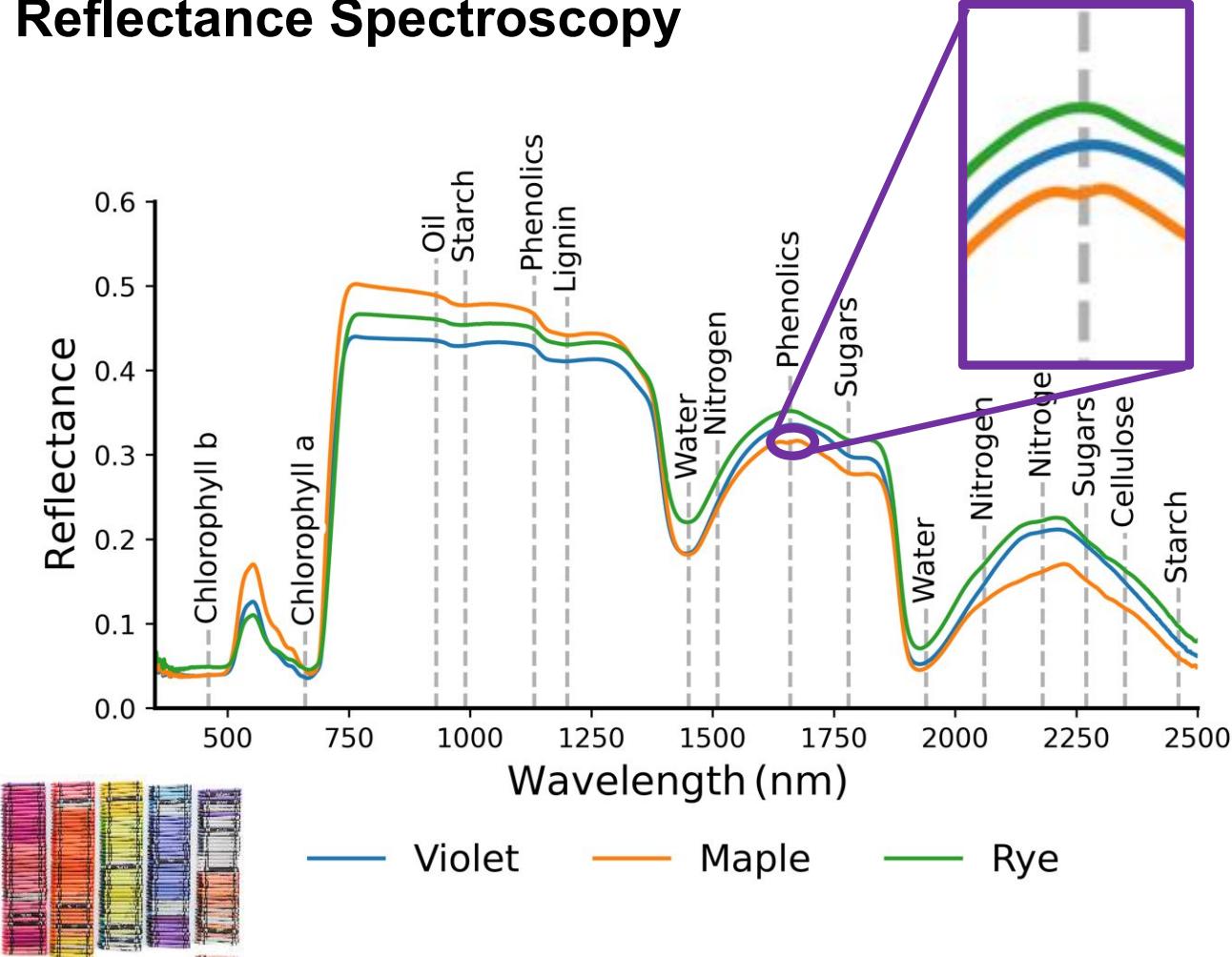
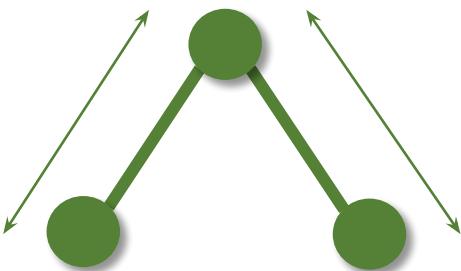


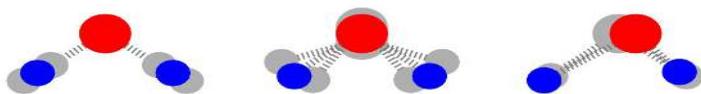
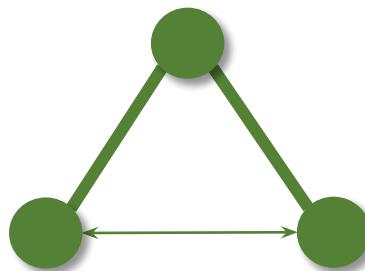
Figure: Adam Chlubas

Vegetation spectroscopy: Why does this work?

Stretching

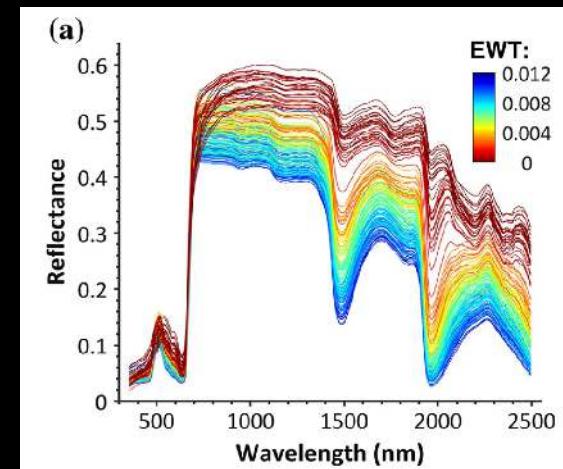
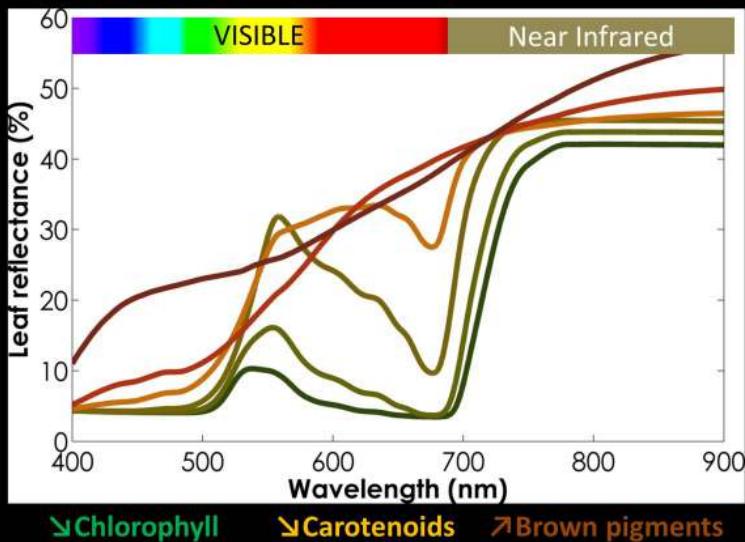


Bending & Twisting



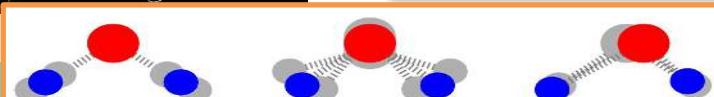
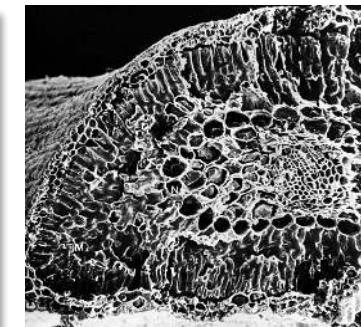
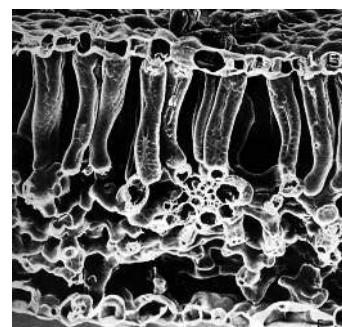
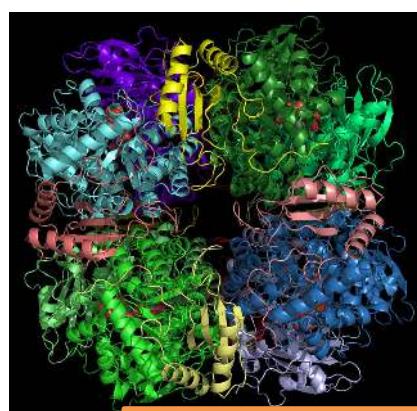
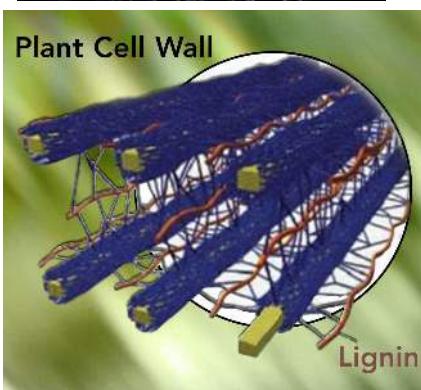
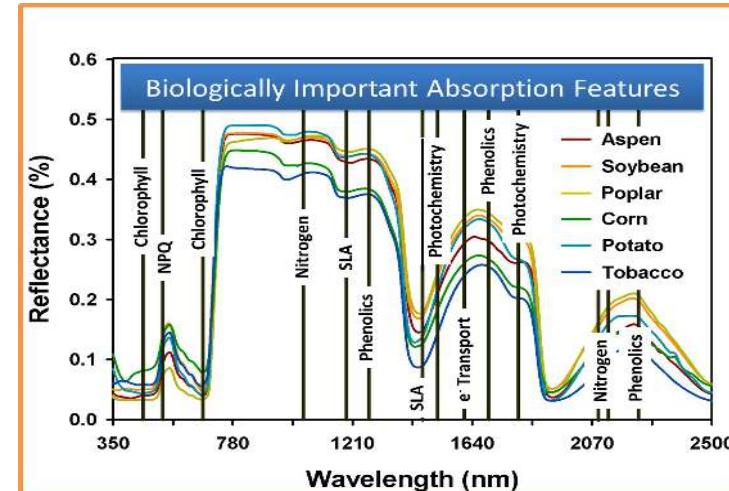
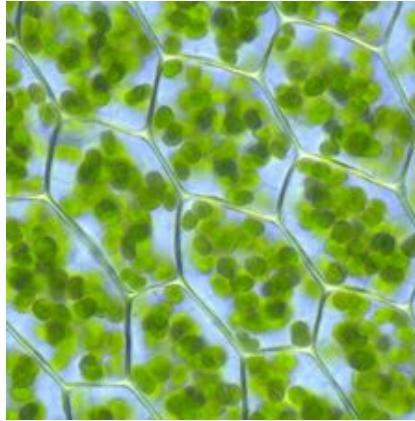
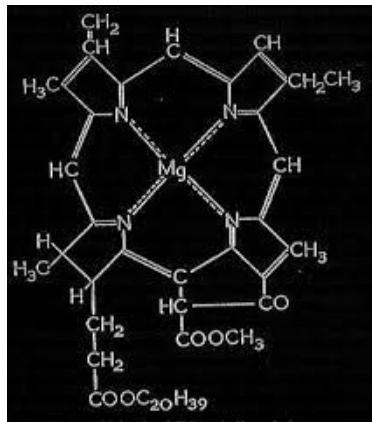
Harmonics of O-H, C-H and N-H stretches

What can leaf/canopy optics

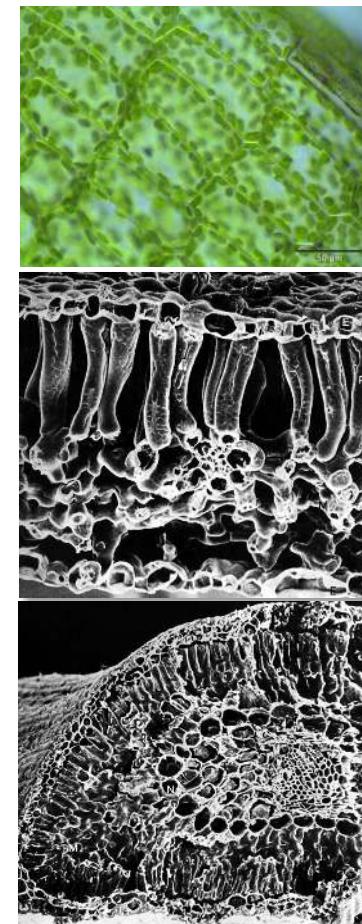
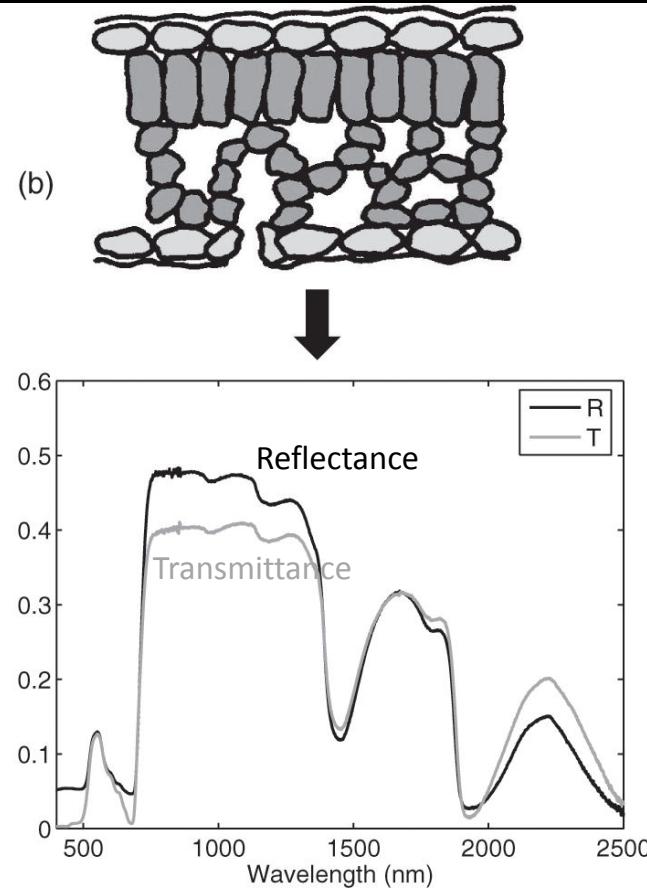
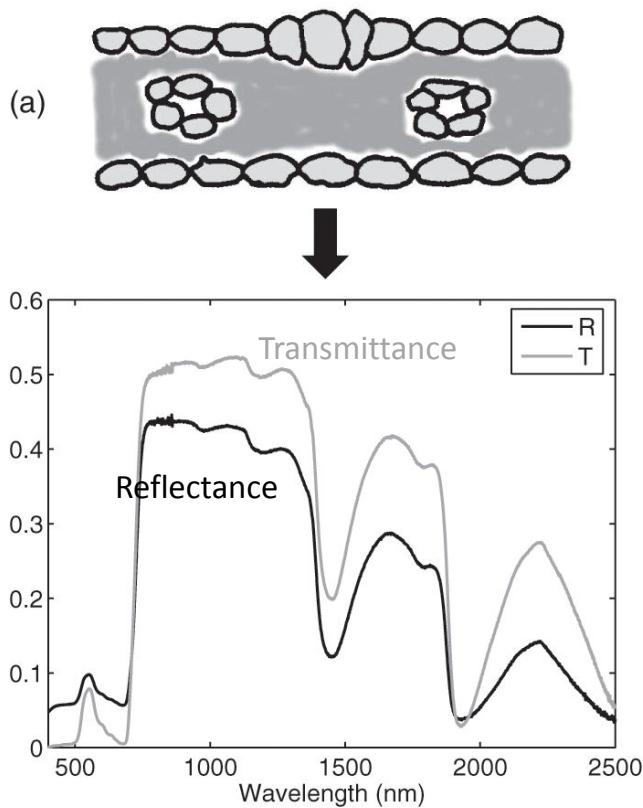


Drying experiment in oak leaves,
Hill et al. 2019

Leaf structure includes leaf constituents



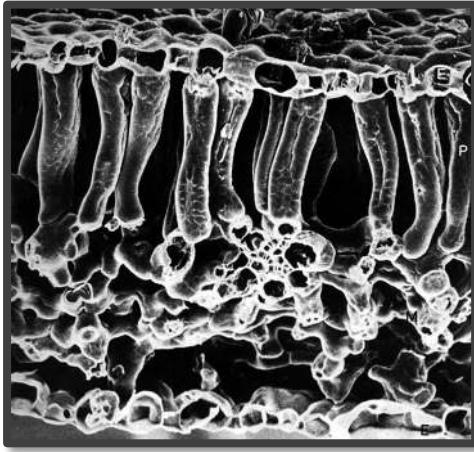
Leaf structure



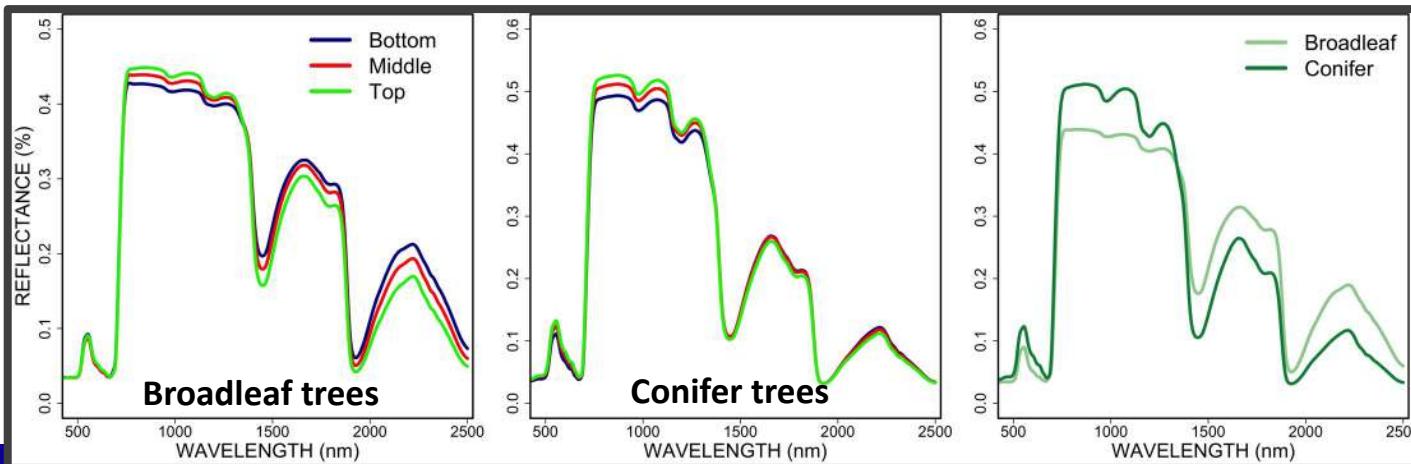
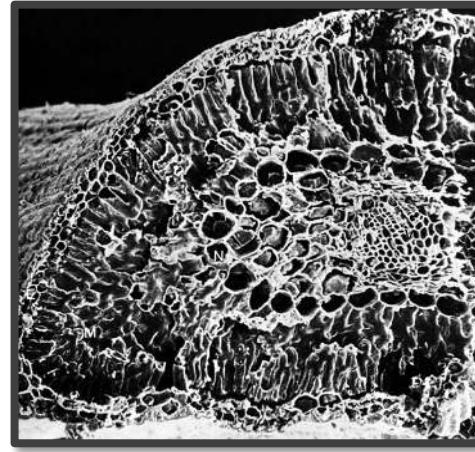
Jacquemoud and Ustin 2019

Leaf structure and spectra (leaf level)

Maple

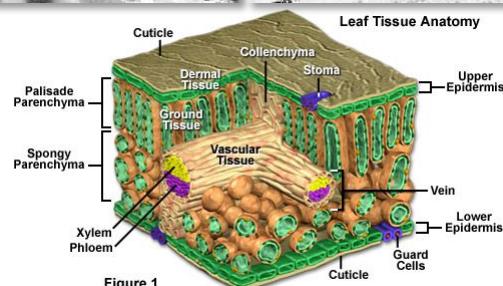
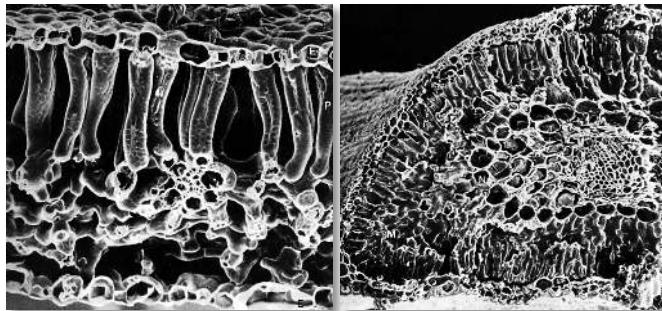
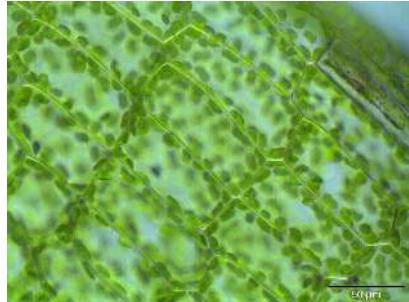


Pine



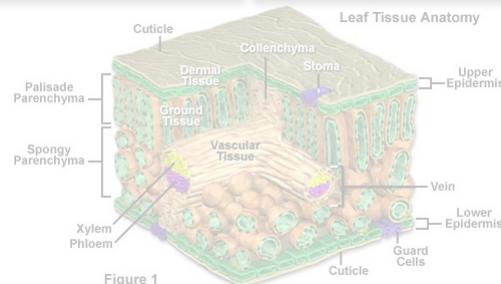
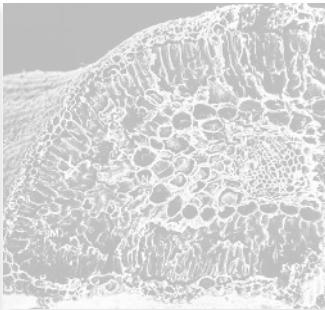
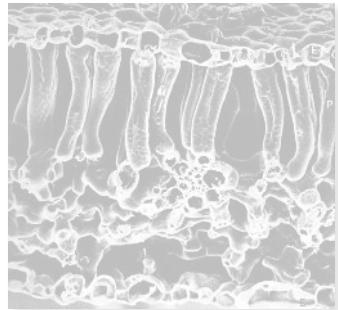
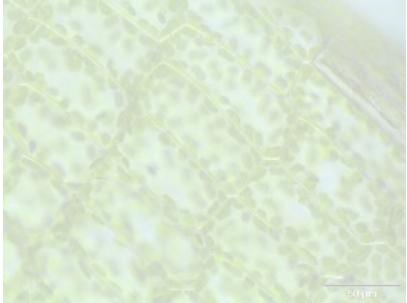
What are plants doing?

What's different among plants?



What are plants doing?

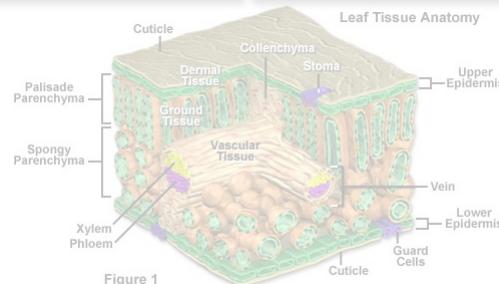
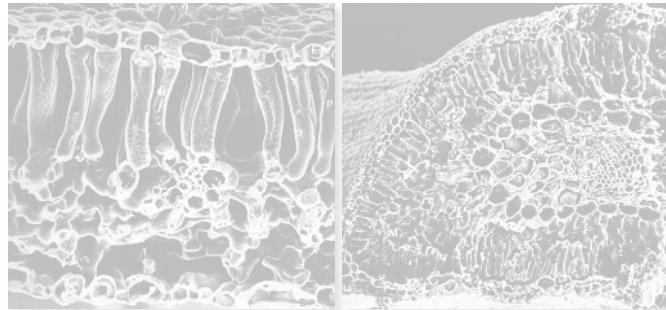
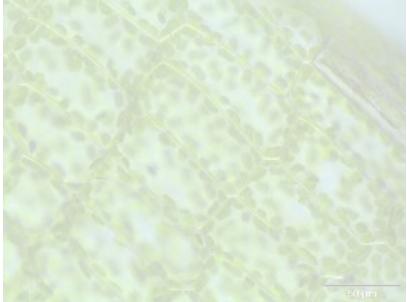
What's different among plants?



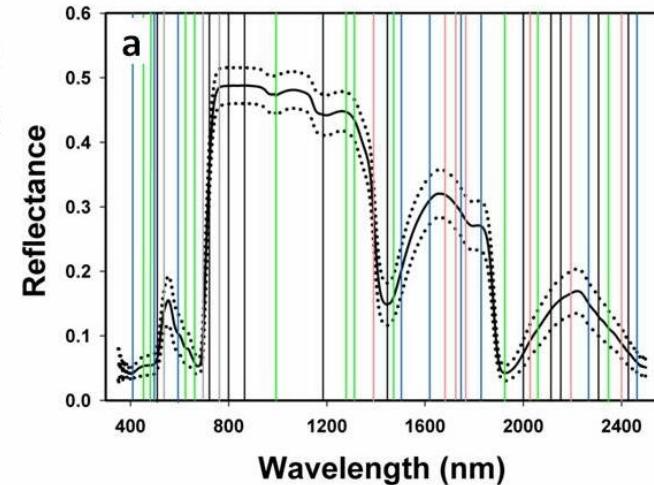
What are foliar functional traits
and why do we care?

What are plants doing?

What's different among plants?

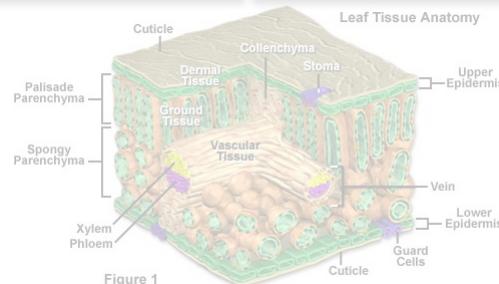
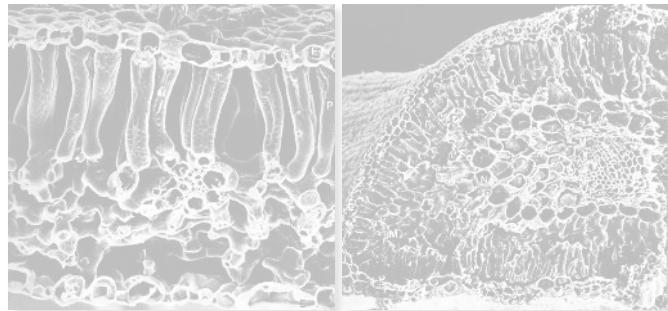
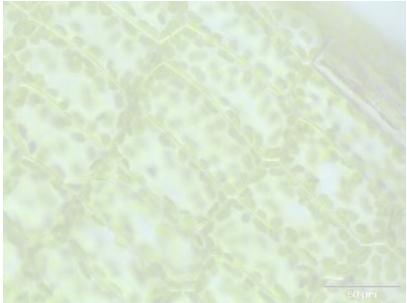


What are foliar functional traits and why do we care?



What are plants doing?

What's different among plants?



Photosynthesis

$\text{CO}_2 \square$ carbohydrates

Nitrogen

Leaf Mass per Area (LMA)

Sugars and Starches

Chlorophyll, Pigments

Water

P, K, Ca, Mg

Decomposition

Structural Compounds

Lignin

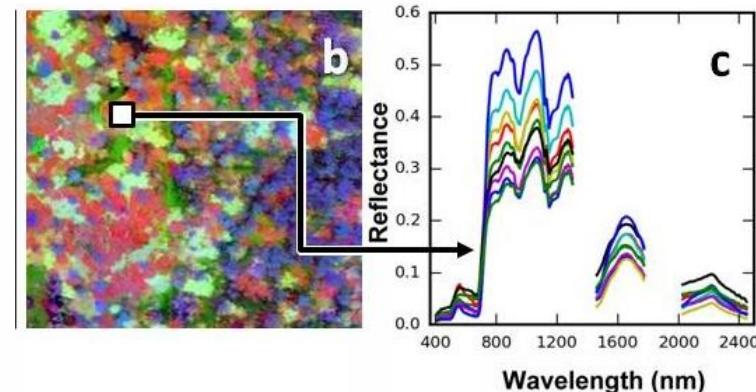
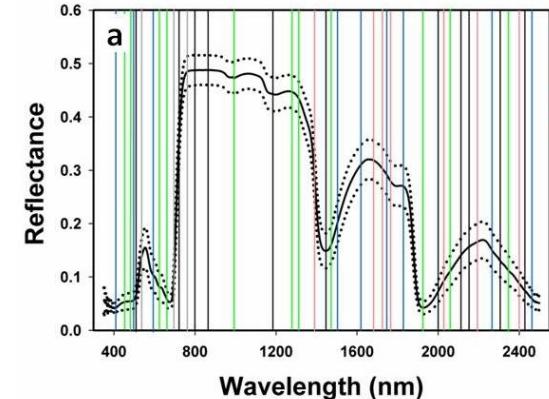
Cellulose

Defense

Tannins

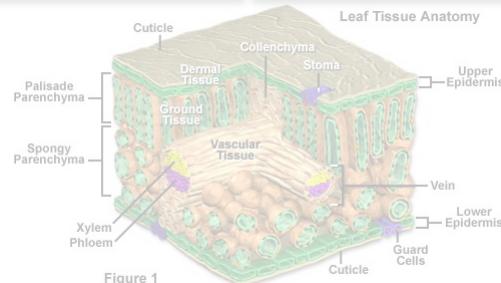
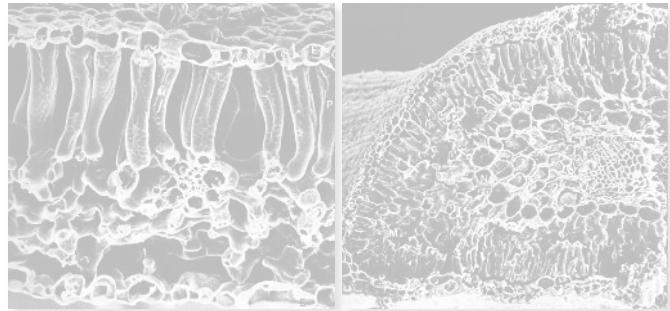
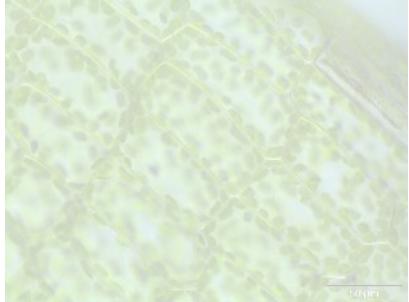
Phenolics

What are foliar functional traits and why do we care?



What are plants doing?

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Photosynthesis

$\text{CO}_2 \square$ carbohydrates

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Leaf Mass per Area
(LMA)

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phenolics

What are foliar functional traits
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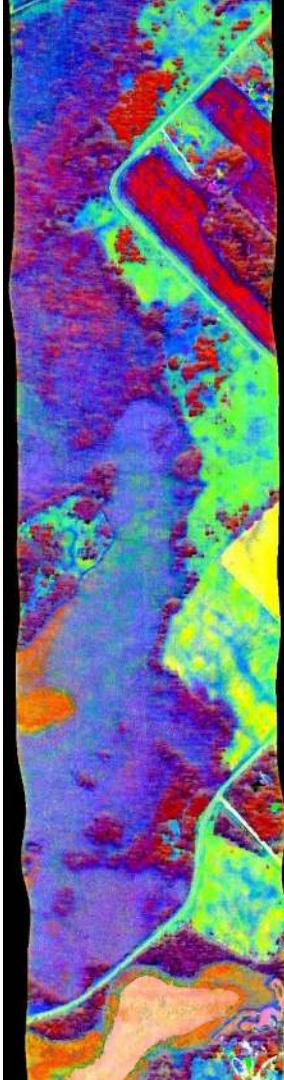
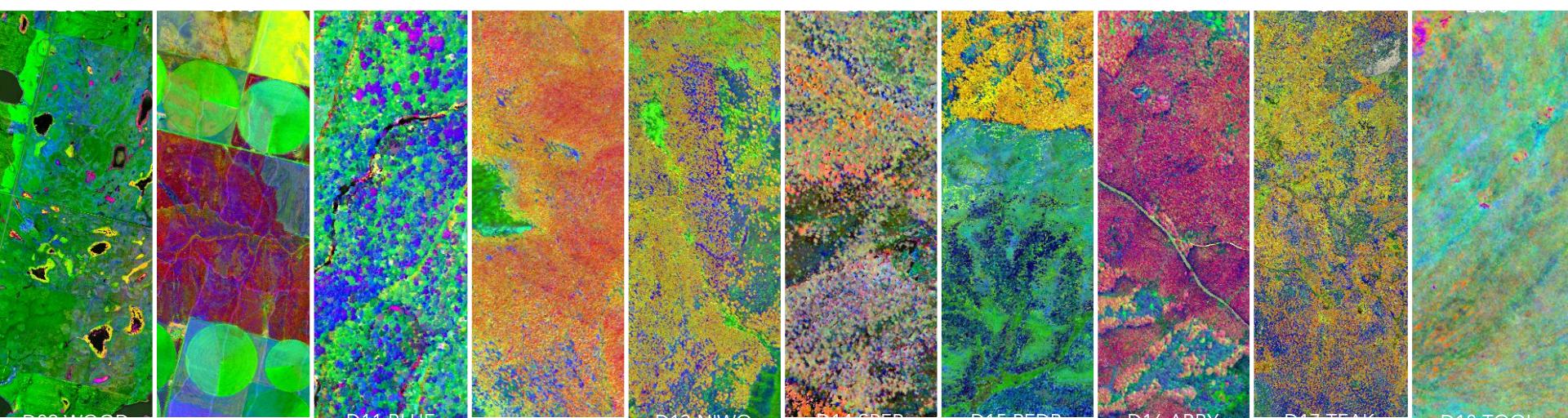
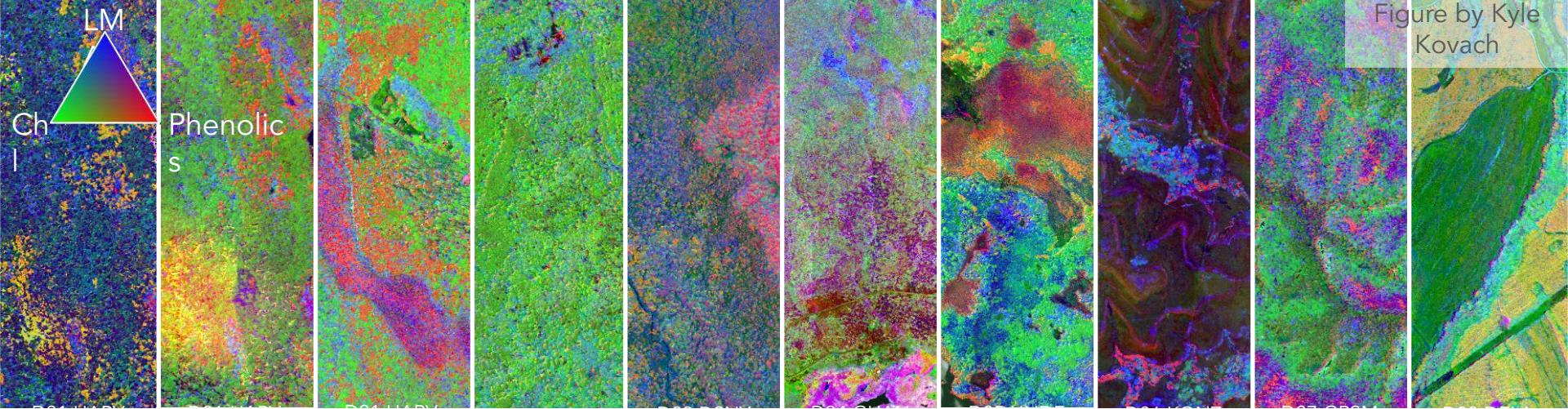
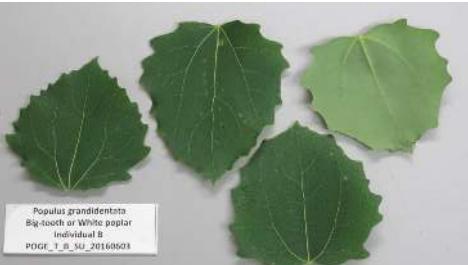
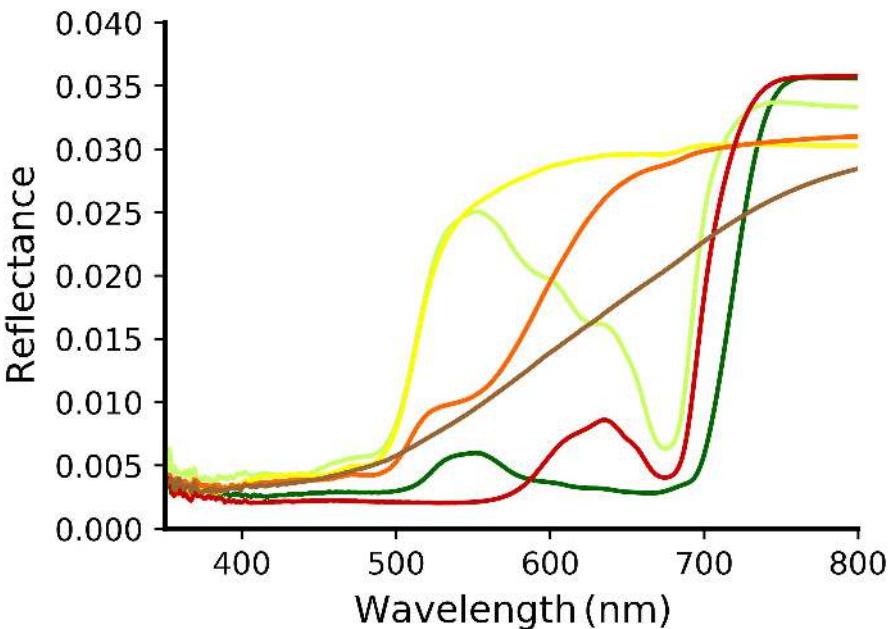




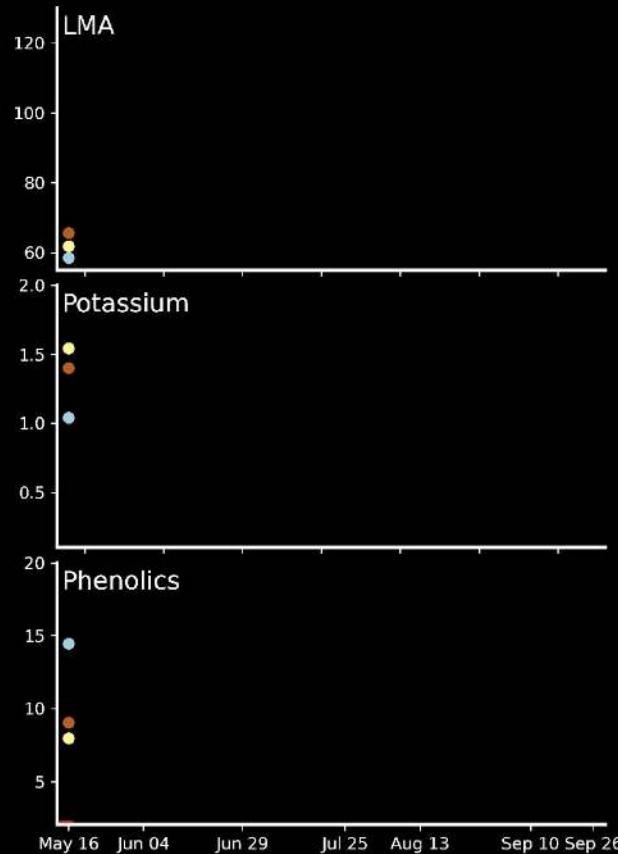
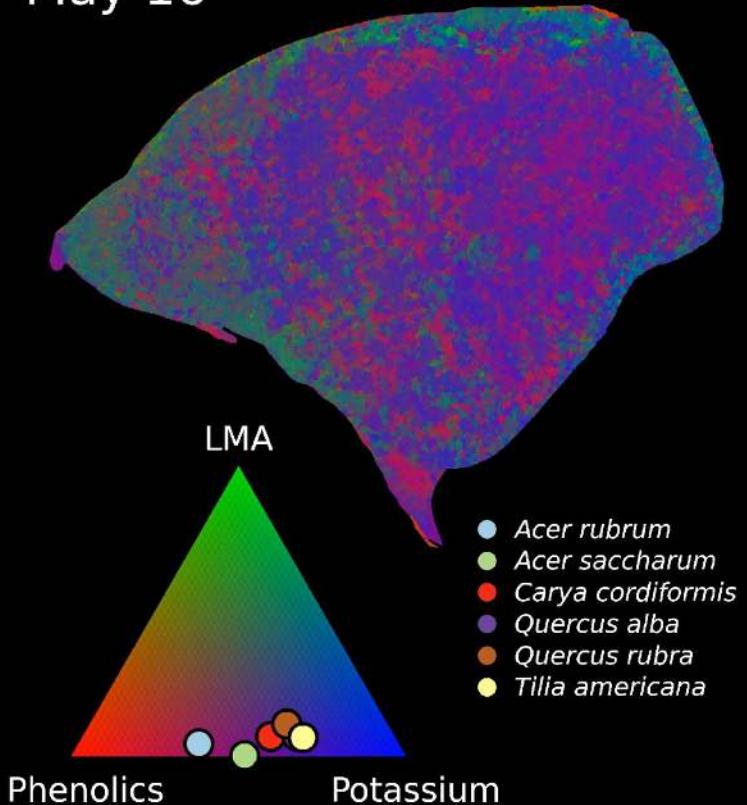
Figure by Kyle Kovach



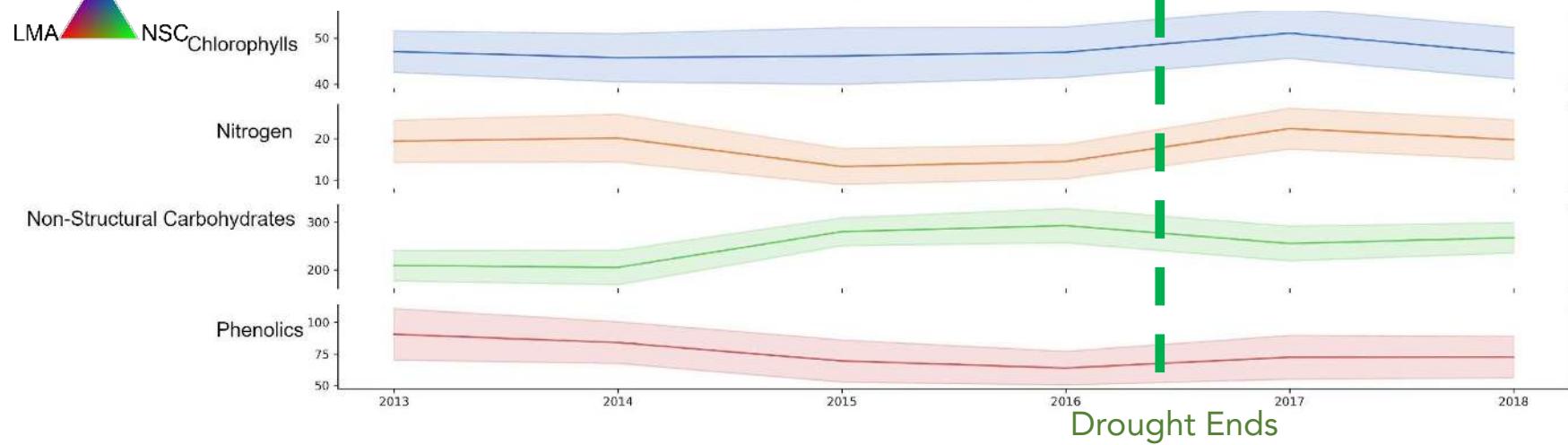
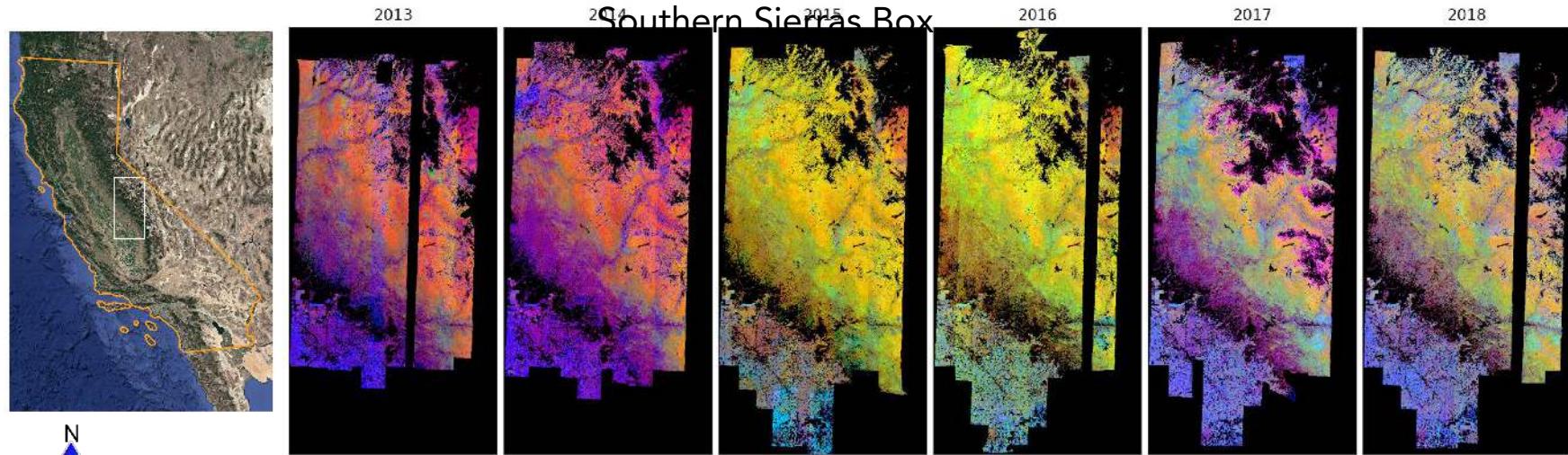
Colors



May 16



Changes in Foliar Functional Traits from AVIRIS-Classic during the California Drought – Yosemite / Southern Sierras Box



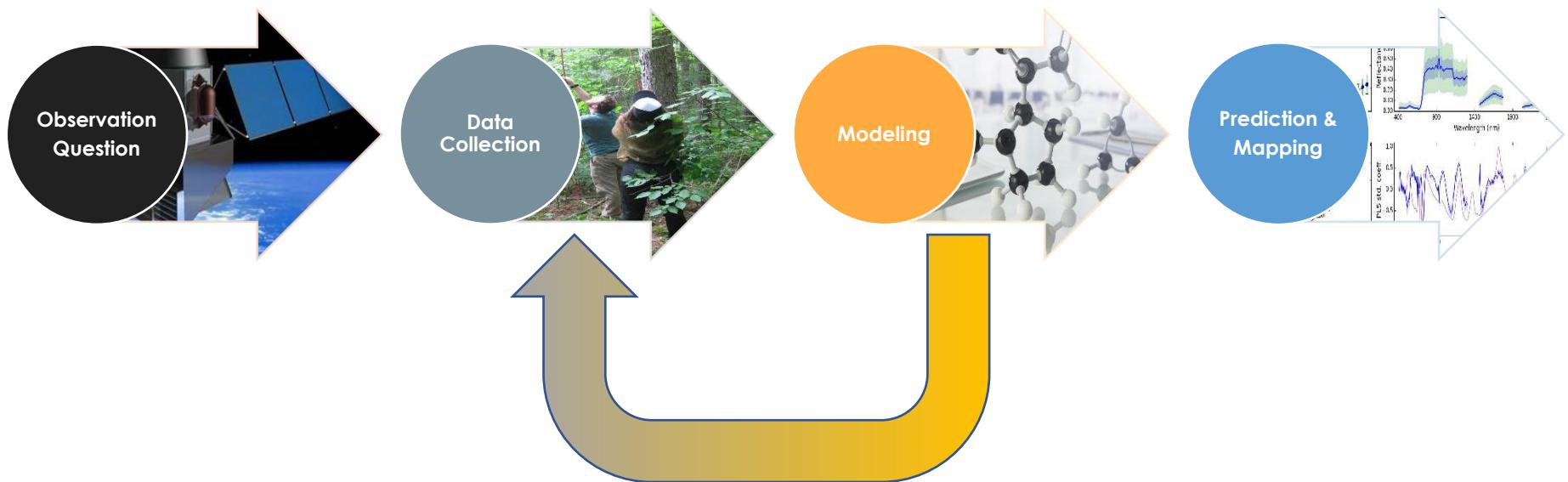
I HAVE QUESTIONS

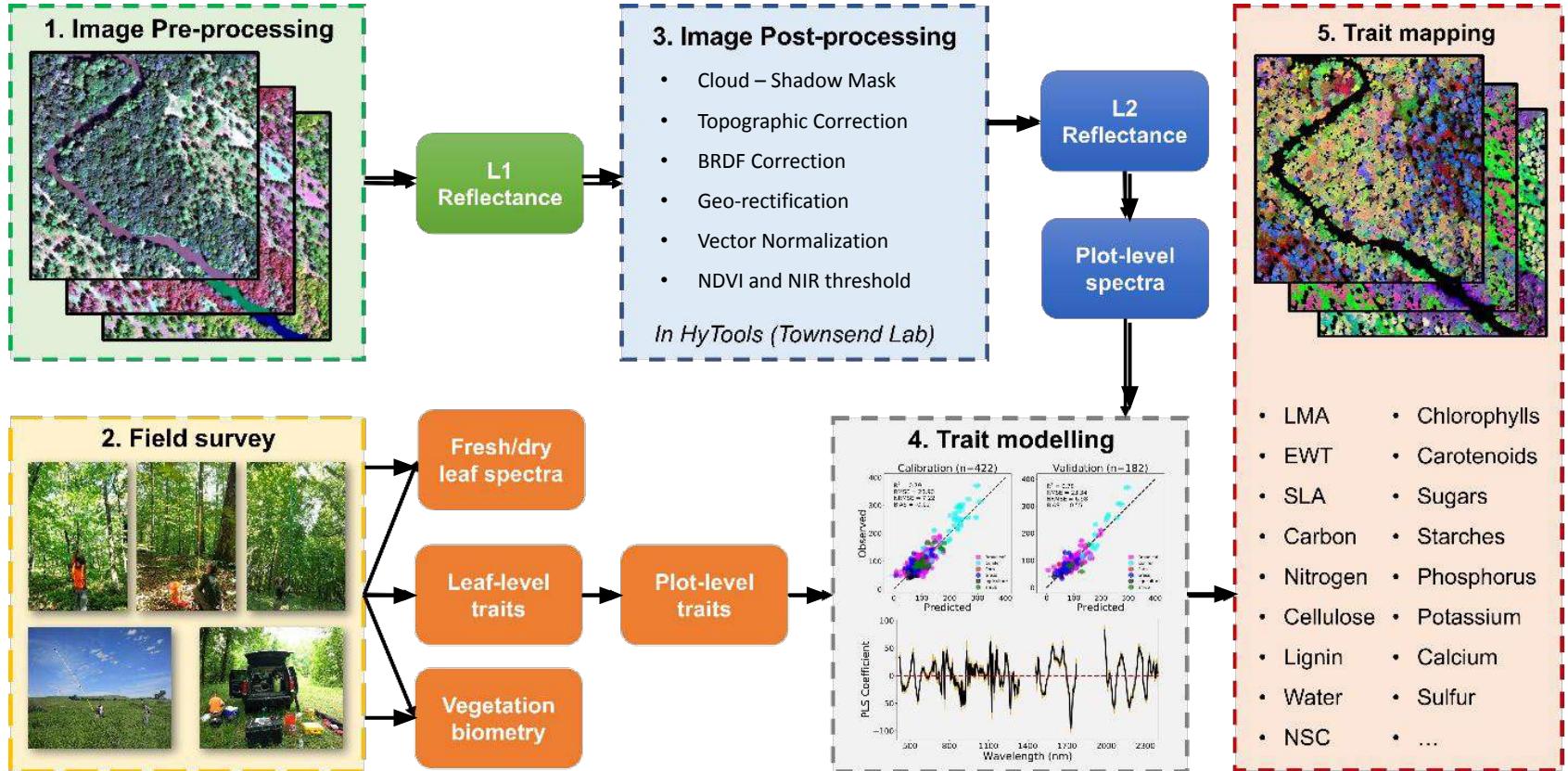
LOTS OF QUESTIONS

How do we map traits from hyperspectral imagery?



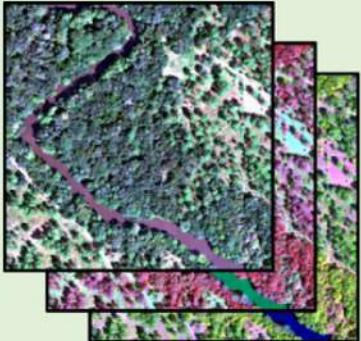
Designing Your Study Using Imaging Spectroscopy





Modeling Overview

1. Image pre-processing



L2
Reflectance

3. Image post-processing

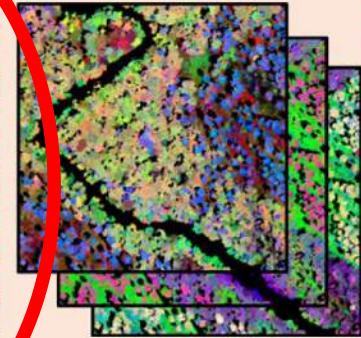
- Cloud - Shadow Mask
- Topographic Correction
- BRDF Correction
- Wavelength Resampling
- Vector Normalization
- NDVI and NIR threshold

In HyTools (Townsend Lab)

L2
Reflectance

Plot-level
spectra

5. Trait mapping



2. Field survey



Fresh/dry
leaf spectra

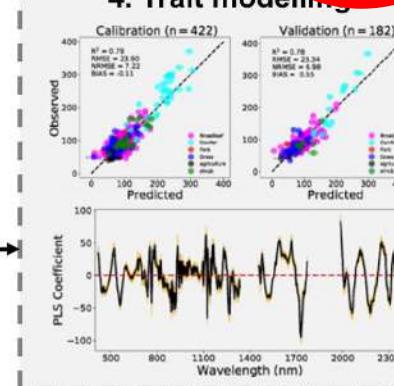
Leaf PLSR
models

Leaf-level
traits

Plot-level
traits

Species
abundance

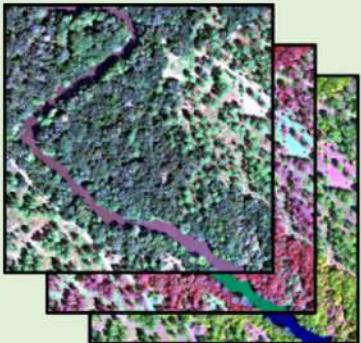
4. Trait modeling



- | | |
|-------------|----------------|
| • LMA | • Chlorophylls |
| • EWT | • Carotenoids |
| • SLA | • Sugars |
| • Carbon | • Starches |
| • Nitrogen | • Phosphorus |
| • Cellulose | • Potassium |
| • Lignin | • Calcium |
| • Water | • Sulfur |
| • NSC | • ... |

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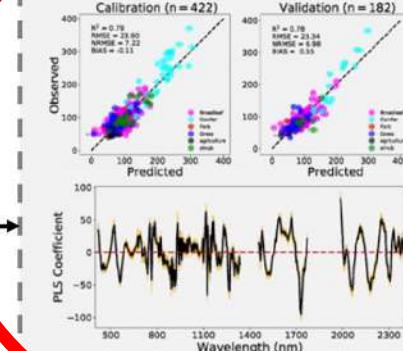
Leaf PLSR
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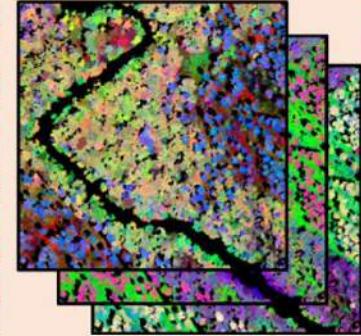
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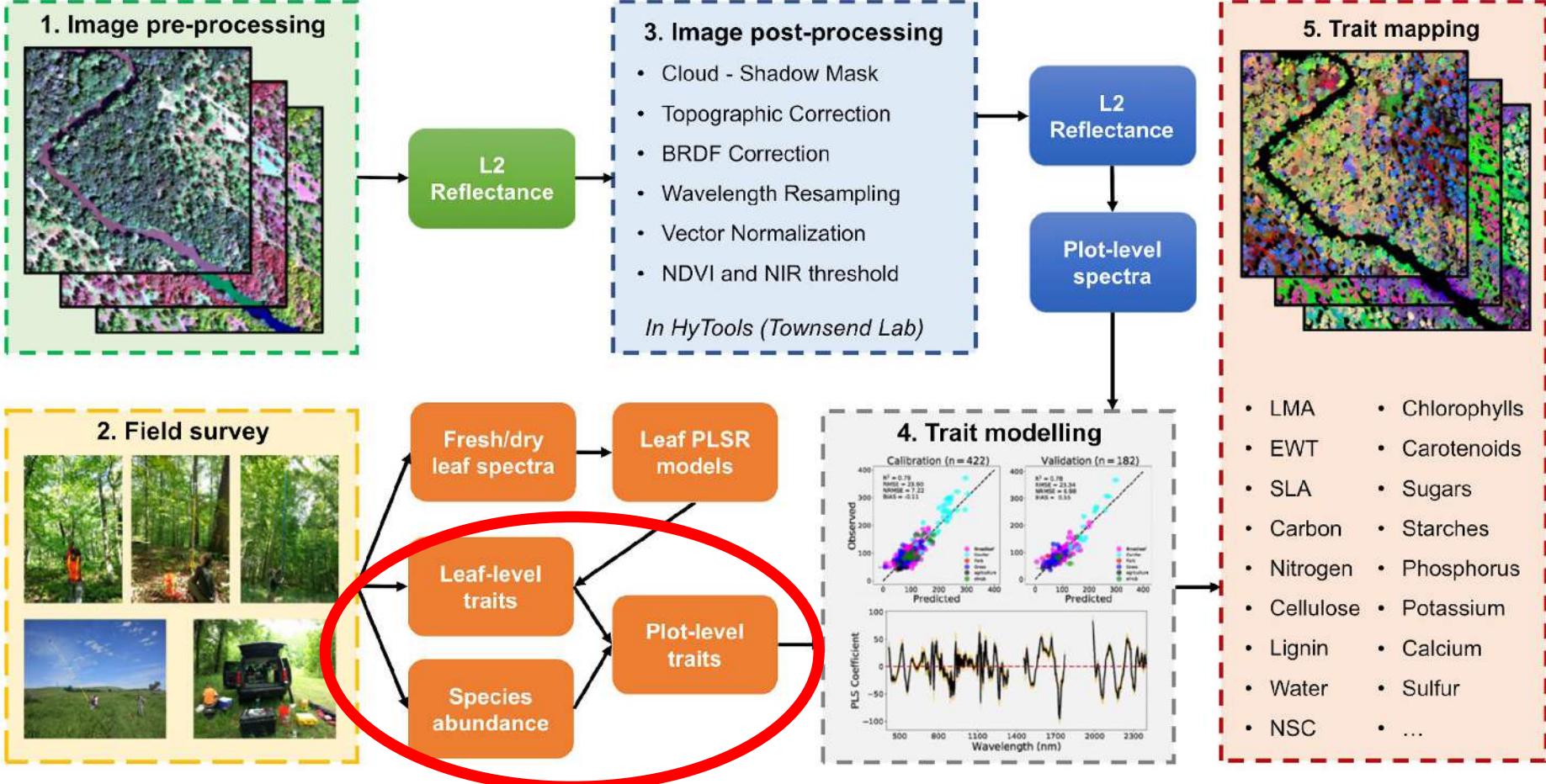


- | | |
|-----------|----------------|
| • LMA | • Chlorophylls |
| • EWT | • Carotenoids |
| • SLA | • Sugars |
| • Carbon | • Starches |
| Nitrogen | • Phosphorus |
| Cellulose | • Potassium |
| • Lignin | • Calcium |
| • Water | • Sulfur |
| • NSC | • ... |

A photograph of a person's hand holding a clear plastic bag filled with green grass seeds against a bright blue sky. The bag is tied at the top with a blue elastic band. The background consists of tall, green grass blades.

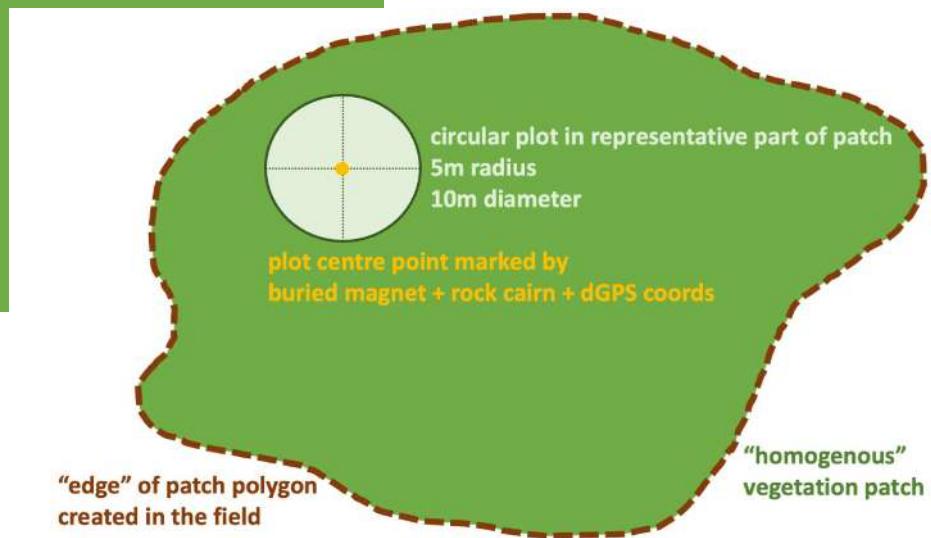
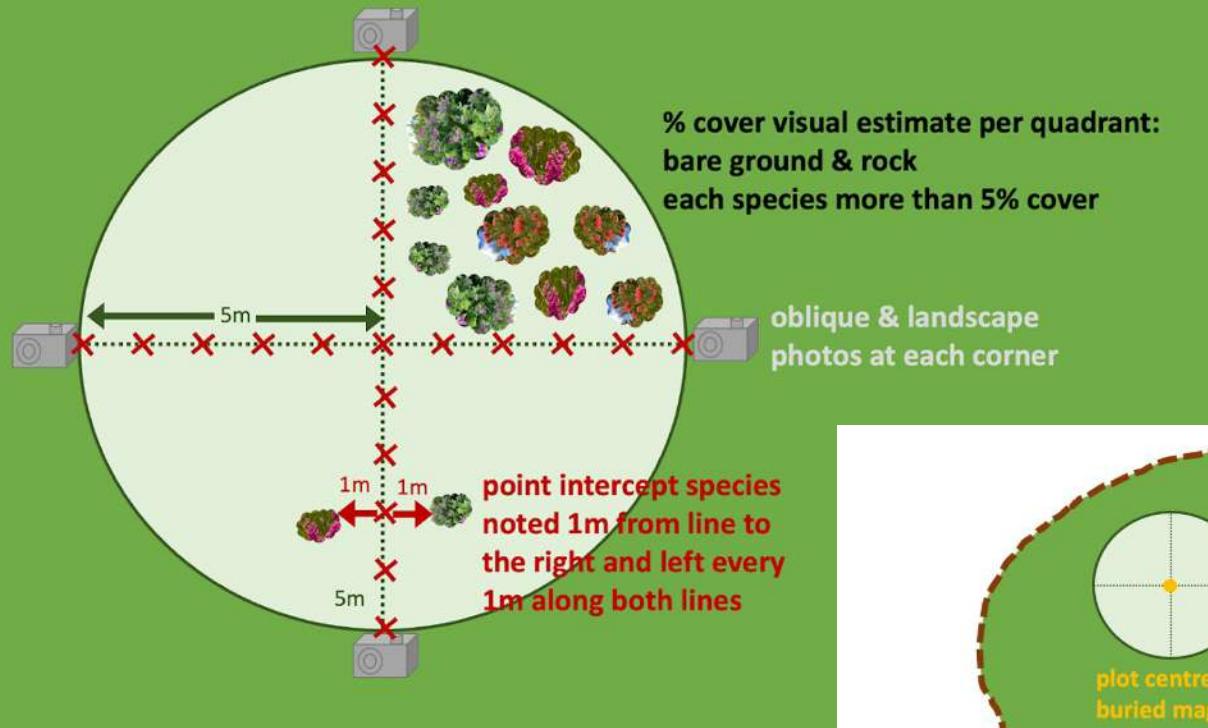
Your Data

Community-Weighted Scaling

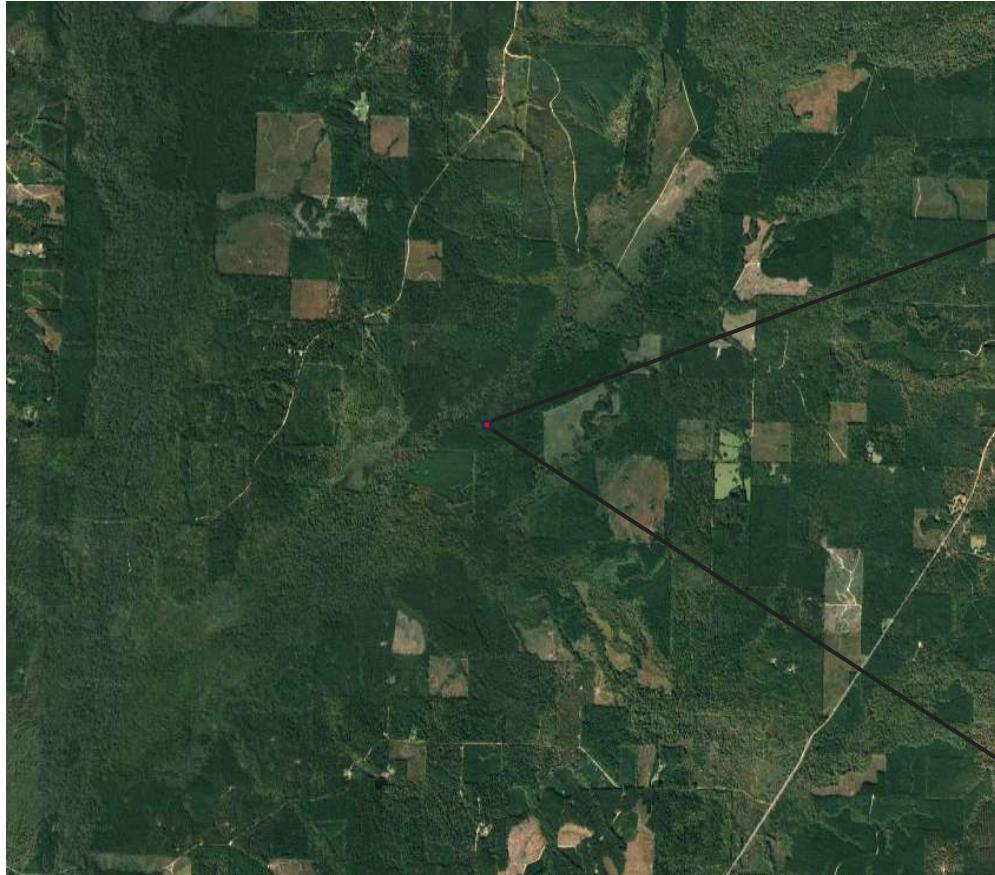


Plot Traits for Remote Sensing

- Community-weighted mean upscaling
 - Many possible definitions
 - Consider what the air/spaceborne sensor “sees”



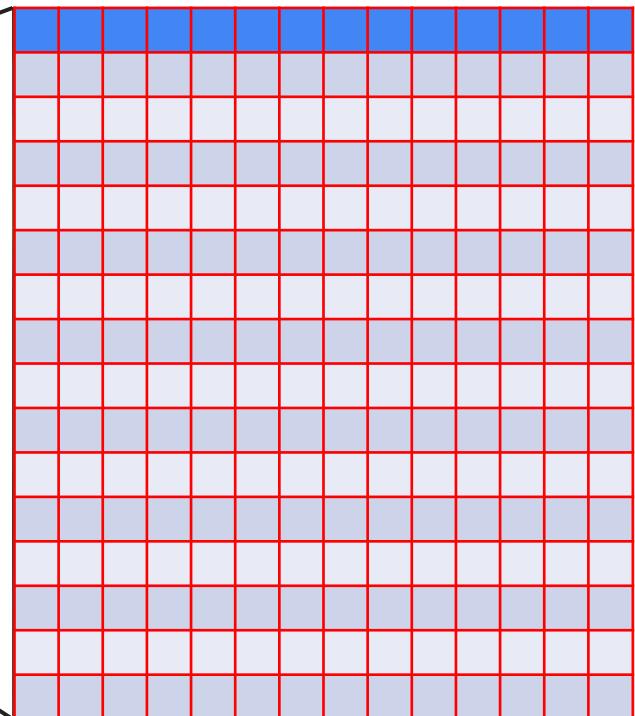
Plot Selection



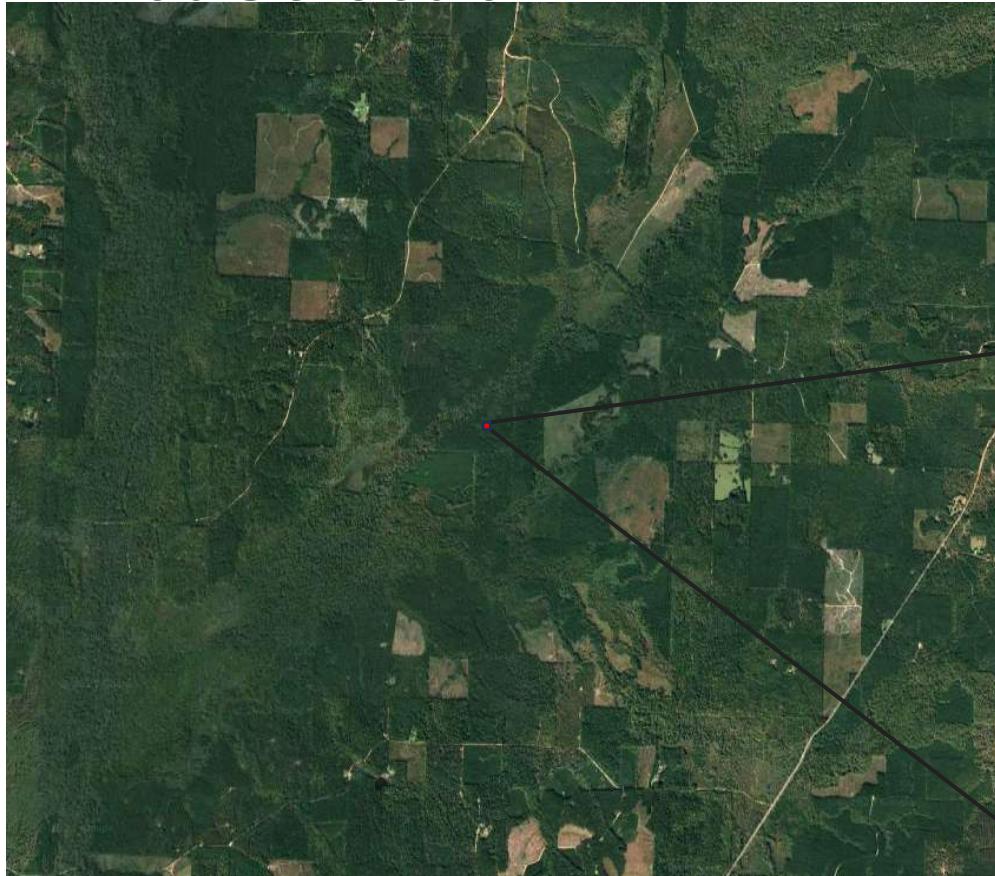
Size: Dim = $P(1+2L)$

P = pixel size (m)

L = location error in # pixels



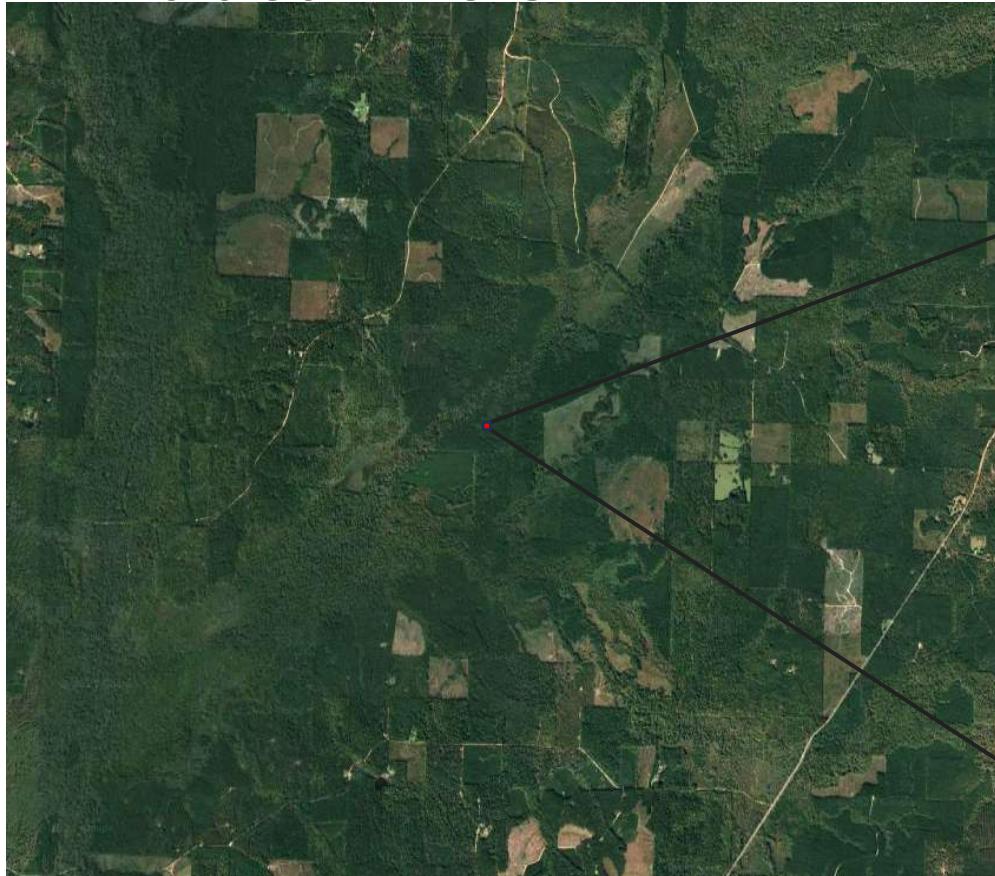
Plot Selection



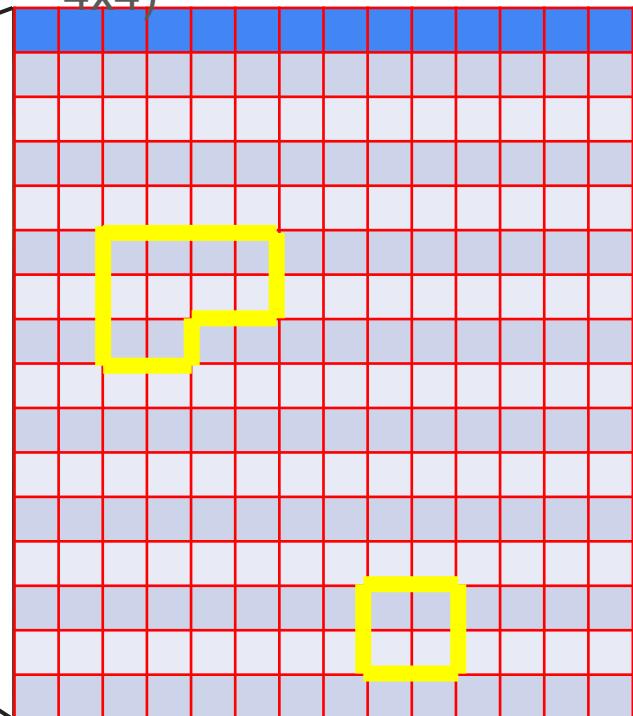
- Plot delineation
- GPS point for center of plot
- Single crown = one trait value
- Multiple species = community weighted mean
- All species with cover greater than 5% adding to at least 80% of total cover



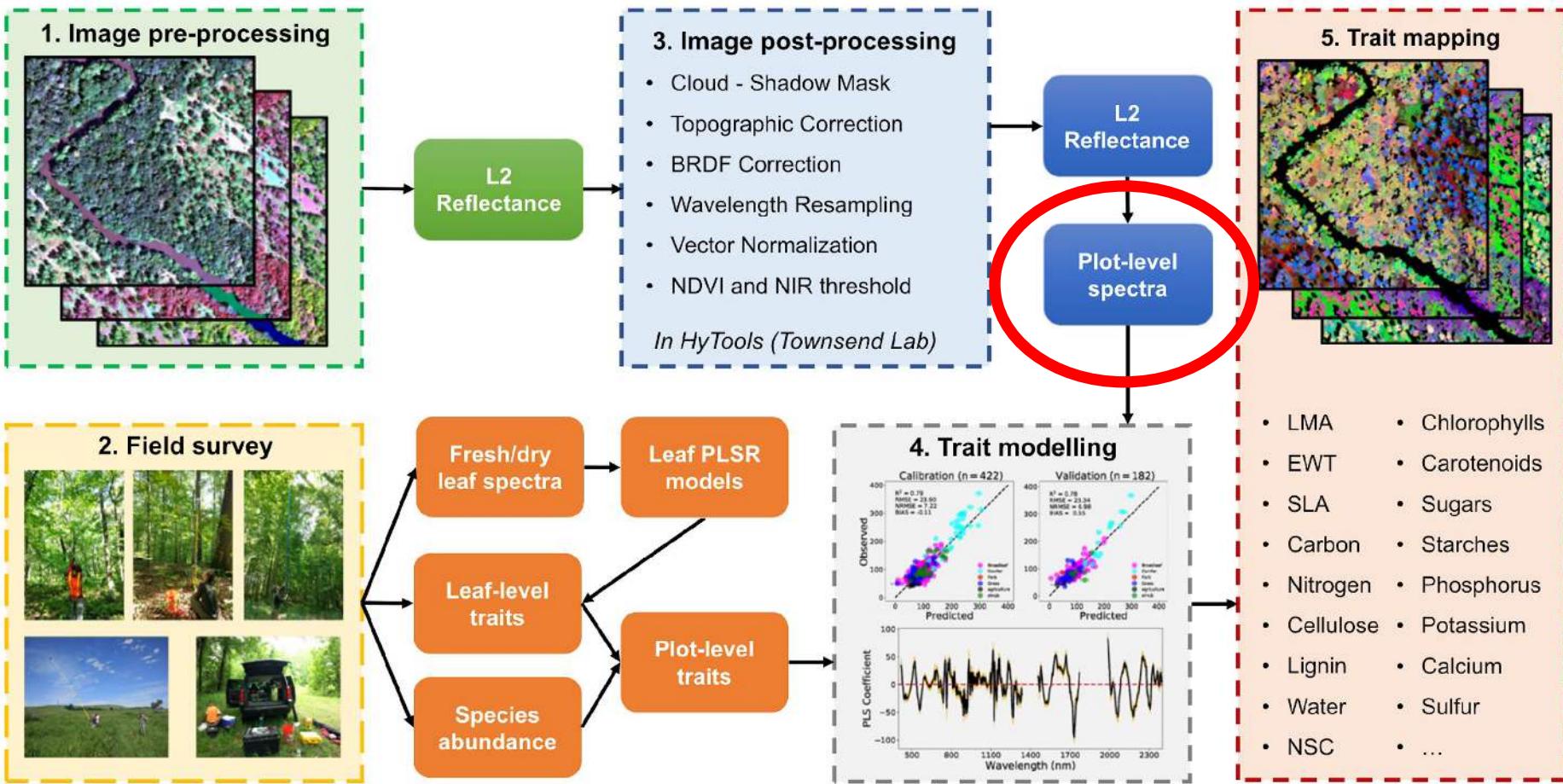
Extract Pixels



- Use crown delineation for extraction
- Or take grid (2×2 , 3×3 , 4×4)



Modeling Overview



Creating Plot Spectra

- Create plot spectra using one of two methodologies

 1. Average pixels (to create non-existent pixel)
 2. Sample from pixels within plot

DON'T PSUEDOREPLICATE!

2340.417	2345.426	2350.436	2355.446	2360.456	2365.465	2370.475	2375.485	2380.495	2385.504	2390.514	2395.524	plotname	site	lon	lat
308	294	312	301	303	270	290	279	276	258	271	260	CHEQ01_PIBA	CHEQ	-90.0727	45.82754
131	121	138	131	134	129	155	127	130	130	134	128	CHEQ01_PIBA	CHEQ	-90.0727	45.82753
399	348	352	372	364	329	346	346	332	317	360	345	CHEQ01_PIBA	CHEQ	-90.0727	45.82753
515	543	492	516	521	511	489	467	444	441	451	461	CHEQ01_PIBA	CHEQ	-90.0727	45.82753
445	418	447	432	465	437	456	438	398	396	399	398	CHEQ01_PIBA	CHEQ	-90.0727	45.82753
136	126	140	144	158	134	177	157	127	137	126	129	CHEQ01_PIBA	CHEQ	-90.0727	45.82752
339	347	347	356	349	312	340	317	310	326	304	277	CHEQ01_PIBA	CHEQ	-90.0727	45.82752
345	354	319	338	332	326	310	296	314	298	280	311	CHEQ01_PIBA	CHEQ	-90.0727	45.82752
423	419	400	390	407	388	406	376	352	332	340	384	CHEQ01_PIBA	CHEQ	-90.0727	45.82752
110	127	105	89	89	110	117	119	122	77	116	105	CHEQ01_PIBA	CHEQ	-90.0727	45.82751
182	199	176	190	172	158	185	155	173	172	146	160	CHEQ01_PIBA	CHEQ	-90.0727	45.82751
108	106	116	113	95	102	92	136	68	78	95	122	CHEQ01_PIRE	CHEQ	-90.0767	45.82908
84	81	81	97	70	85	87	79	76	89	76	59	CHEQ01_PIRE	CHEQ	-90.0767	45.82908
153	148	155	152	146	110	122	140	99	115	110	150	CHEQ01_PIRE	CHEQ	-90.0767	45.82907
97	106	104	94	97	91	130	105	94	91	68	90	CHEQ01_PIRE	CHEQ	-90.0767	45.82907
82	83	105	85	103	86	86	104	86	82	97	99	CHEQ01_PIRE	CHEQ	-90.0767	45.82907
271	270	257	250	245	242	279	202	224	222	221	202	CHEQ01_PIRE	CHEQ	-90.0767	45.82906
135	132	133	145	115	115	164	123	108	160	122	118	CHEQ01_PIRE	CHEQ	-90.0767	45.82906
140	134	94	117	110	108	140	120	94	81	101	103	CHEQ01_PIRE	CHEQ	-90.0767	45.82906
307	263	264	261	257	255	261	239	233	226	225	240	CHEQ02_POTR	CHEQ	-90.0729	45.8285
226	203	181	198	213	199	203	182	161	155	140	161	CHEQ02_POTR	CHEQ	-90.0729	45.8285
258	238	217	231	213	219	186	229	194	204	215	199	CHEQ02_POTR	CHEQ	-90.0729	45.82849
216	231	183	196	204	224	190	226	187	170	175	179	CHEQ02_POTR	CHEQ	-90.0729	45.82849
399	385	376	376	364	343	355	331	318	297	288	297	CHEQ02_POTR	CHEQ	-90.0729	45.82849
255	236	232	230	224	180	209	201	190	187	206	189	CHEQ02_POTR	CHEQ	-90.0729	45.82849
253	245	231	247	220	240	255	218	210	180	204	194	CHEQ02_POTR	CHEQ	-90.0729	45.82849
409	393	381	390	366	340	337	344	332	334	347	309	CHEQ02_POTR	CHEQ	-90.0729	45.82849
385	383	383	396	381	354	363	349	310	305	323	316	CHEQ02_POTR	CHEQ	-90.0729	45.82848
379	362	368	372	349	351	351	337	320	298	313	287	CHEQ02_POTR	CHEQ	-90.0729	45.82848
425	397	382	382	378	363	387	341	358	360	354	327	CHEQ02_POTR	CHEQ	-90.0729	45.82848
376	345	364	382	357	336	369	340	339	342	308	291	CHEQ02_POTR	CHEQ	-90.0729	45.82848
372	369	382	333	333	340	348	321	287	292	299	288	CHEQ02_POTR_low	CHEQ	-90.0903	45.82448

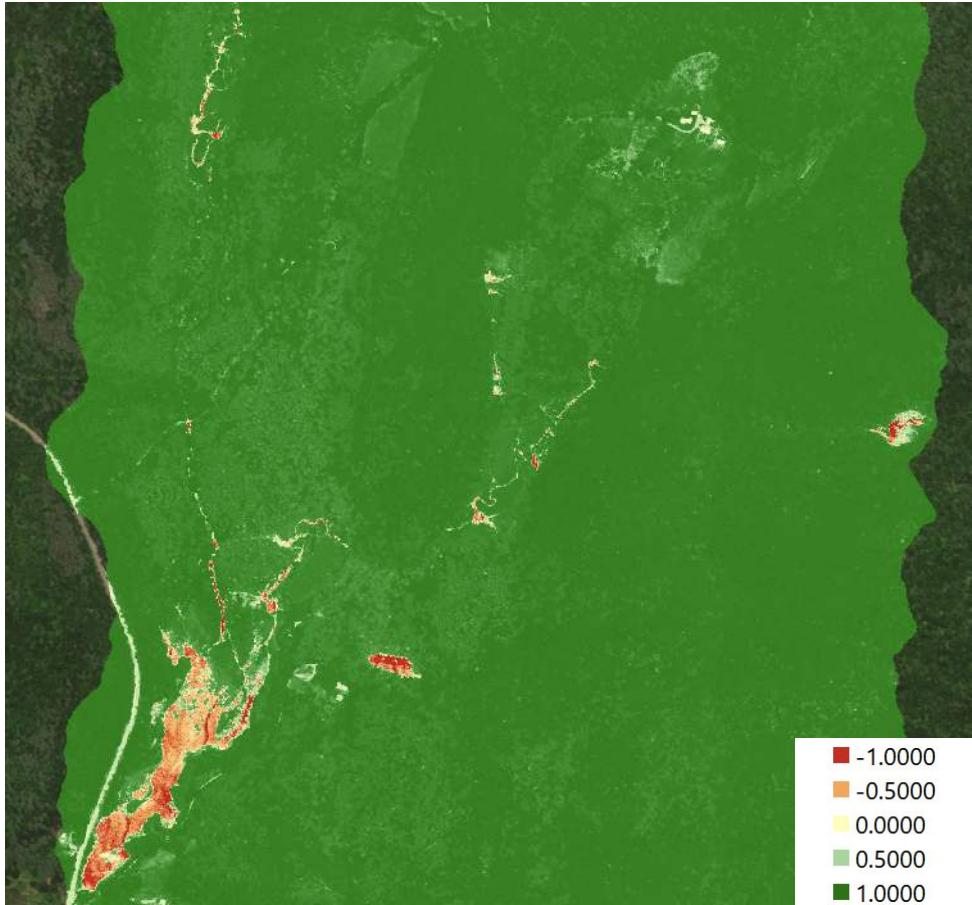
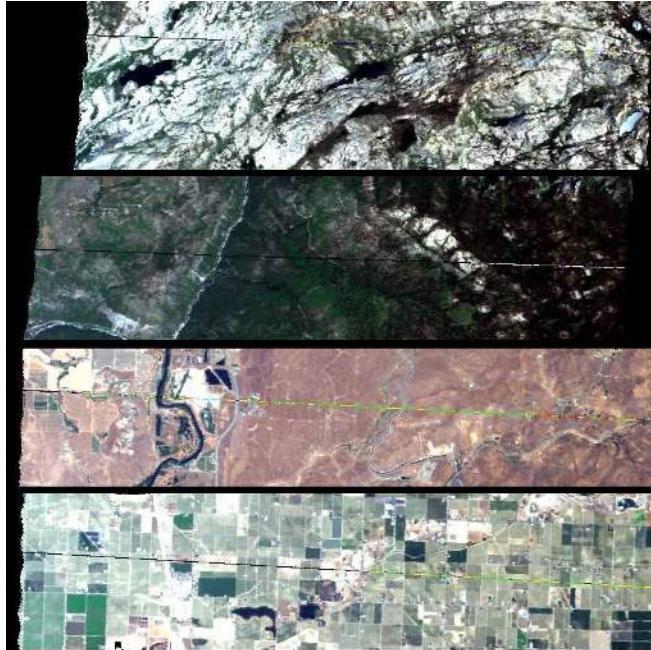
Avg Plot
CHEQ01_PIB
A

Avg Plot
CHEQ01_PIR
E

Avg Plot
CHEQ02_POT
R

Data Quality

- Refining data to build models
1. Assess outliers
 2. Remove non-veg pixels with NDVI threshold
 3. Remove potential shadow pixels with NIR threshold



```
def build_model(trait_name, n_outer, n_inner):
    init_transforms = [htt.LabelBasedSelector(column_name='pix_pos', column_labels='Center'), ## need missing_ok arg
                      htt.SubSampler(),
                      htt.WavelengthSelector(wanted_ranges=[(419.9, 1315.1), (1464.9, 1765.1), (1989.9, 2395.1)]),
                      htt.UnitMagnitudeNormalizer()]
    init_transform = htt.SpectrumDataTransformSequence(init_transforms)
    dataset = htt.SpectrumFrameDataset(data_csv=clean_dir/f'{trait_name}.csv',
                                         transform=init_transform)

    splitter = htt.SpectrumFrameDatasetSplitter(outer_params=htt.SPLIT_PARAMS_SHUFFLE(n_splits=n_outer, percent=80),
                                                calib_inner_params=htt.SPLIT_PARAMS_SHUFFLE(n_splits=n_inner, percent=80),
                                                deploy_inner_params=htt.SPLIT_PARAMS_ALLINONE(percent=100))
    split_data = splitter(sample_ids=dataset.sample_data()[0],
                          sample_labels=dataset.sample_data()[1])

    start_time = time.perf_counter()
    oi_n_comps, oi_rmses, oi_r2s, oi_biases = [], [], [], []
    oi_mnrmsses, oi_qnrmsses, oi_rnr:
```

Modeling

```
        for oi in range(n_outer):
            calib_train_transform = ht.
            calib_train_dataloader = ht.
                split_data=split_data[oi].all_calib_trains(),
                transform=calib_train_transform)

            calib_valid_transform = htt.SpectrumDataTransformSequence([])
            calib_valid_dataloader = htt.SpectrumFrameDatasetDataLoader(dataset=dataset,
                split_data=split_data[oi].all_calib_valids(),
                transform=calib_valid_transform)

            deploy_train_transform = htt.SpectrumDataTransformSequence([])
            deploy_train_dataloader = htt.SpectrumFrameDatasetDataLoader(dataset=dataset,
                split_data=split_data[oi].all_deploy_trains(),
                transform=deploy_train_transform)

            test_transform = htt.SpectrumDataTransformSequence([])
            test_dataloader = htt.SpectrumFrameDatasetDataLoader(dataset=dataset,
                split_data=split_data[oi].all_tests(),
                transform=test_transform)
```

Methods

Surv Geophys (2019) 40:589–629
<https://doi.org/10.1007/s10712-018-9478-y>



Quantifying Vegetation Biophysical Variables from Imaging Spectroscopy Data: A Review on Retrieval Methods

Jochem Verrelst¹ · Zbyněk Malenovský^{2,3,4} · Christiaan Van der Tol⁵ ·
Gustau Camps-Valls¹ · Jean-Philippe Gastellu-Etchegorry⁶ · Philip Lewis^{7,8} ·
Peter North⁹ · Jose Moreno¹

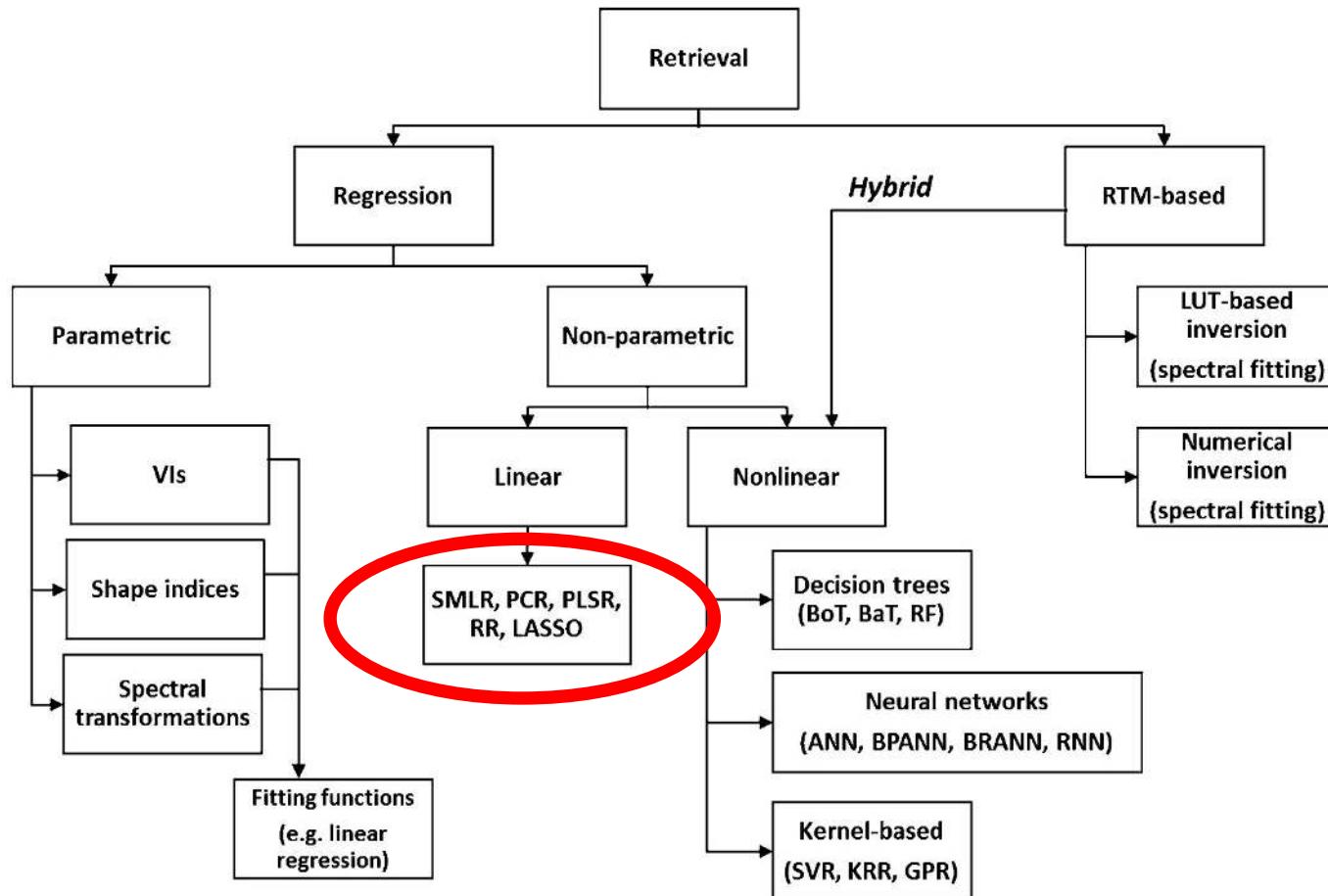
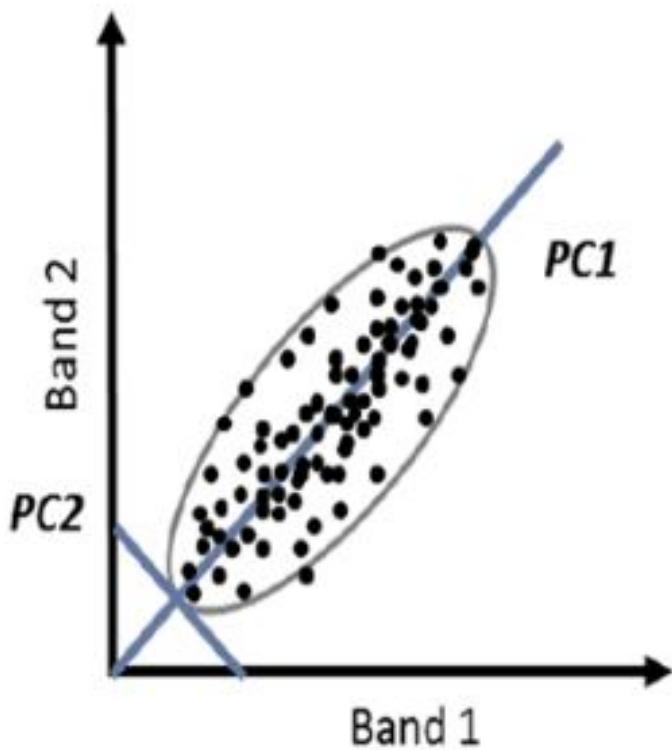


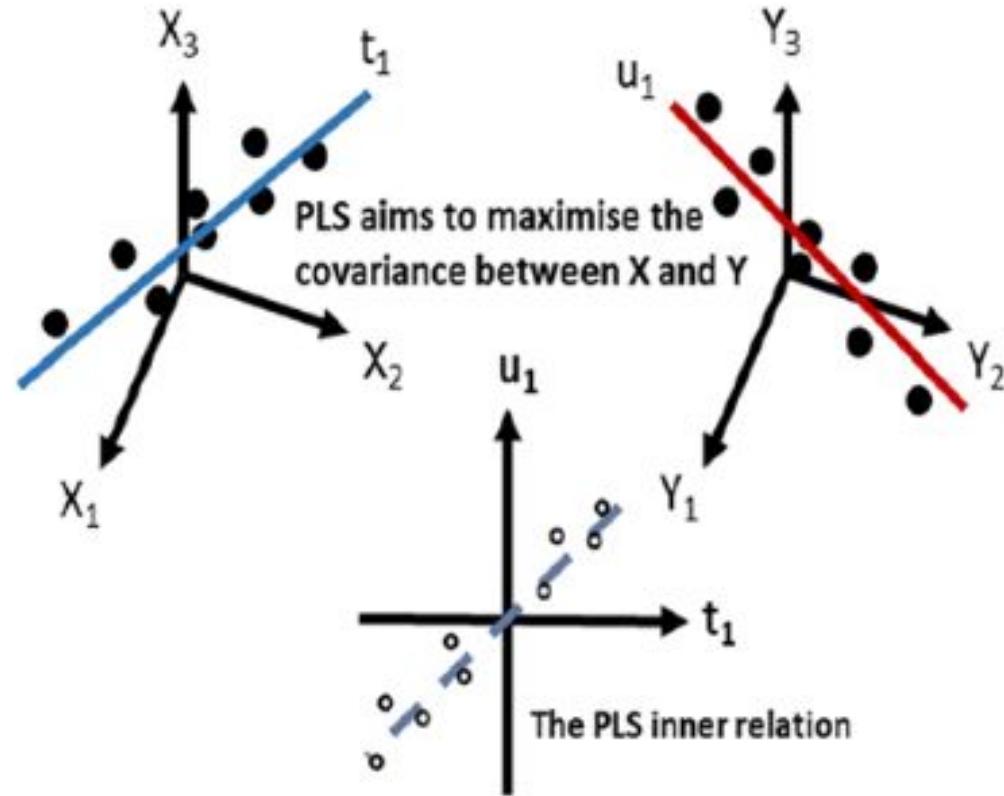
Fig. 9 Schematic overview of the main retrieval methods

Verrelst et al. 2019

PCA (a)



PLS (b)



PLS: Projection to Latent Structures, a.k.a. PLSR: Partial-Least-Squares Regression

Similar to PCA, but...

- maximizes covariance, instead of minimizing correlation
- incorporates the response variable, not just the predictors

Unlike OLS regression, does not assume predictors are error-free

Similar to Multiple Linear Regression, but handles predictor collinearity

able to handle many predictor variables with few response variables

$$\begin{bmatrix} W_{1,1} & \cdots & W_{m,1} \\ \vdots & \ddots & \vdots \\ W_{1,n} & \cdots & W_{m,n} \end{bmatrix} \begin{bmatrix} \beta_1 \\ \vdots \\ \beta_m \end{bmatrix} = \begin{bmatrix} V_1 \\ \vdots \\ V_n \end{bmatrix}$$

Reflectance Spectroscopy

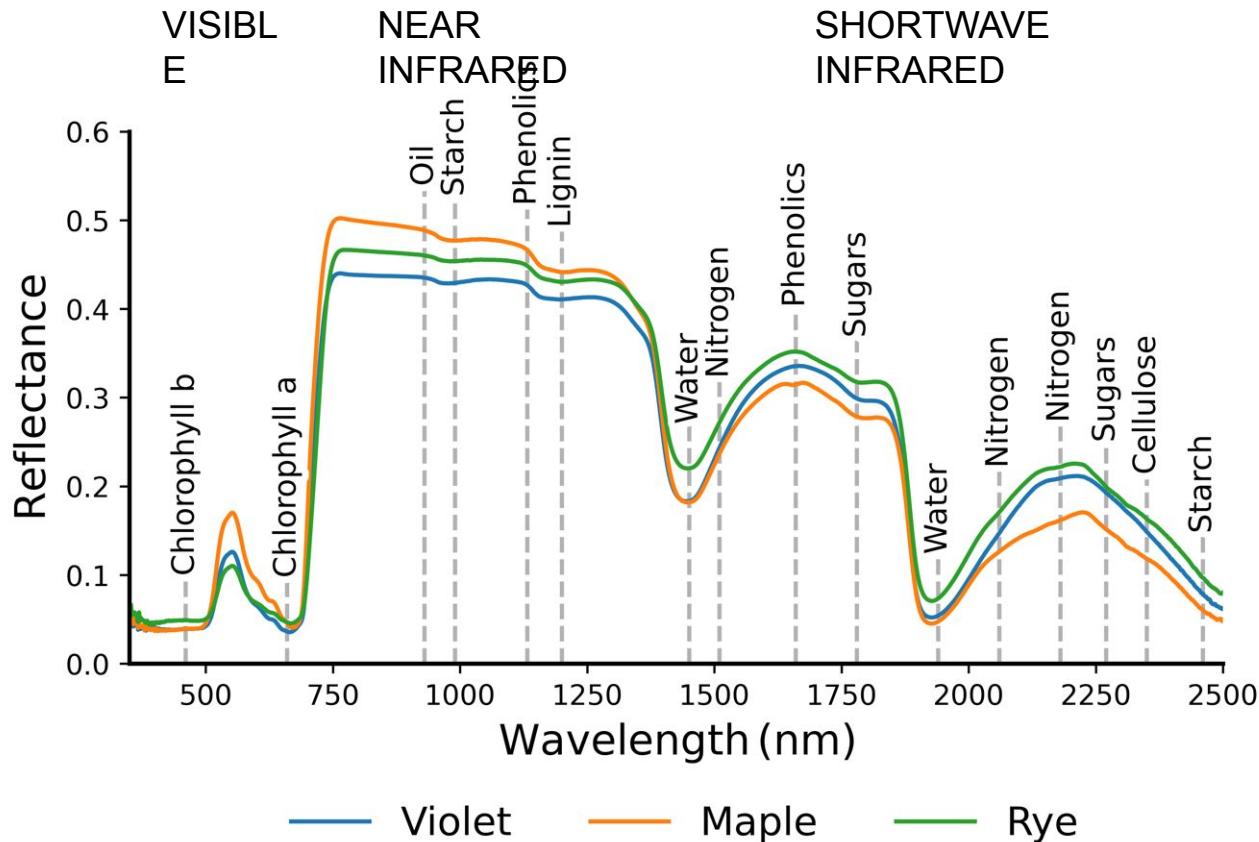
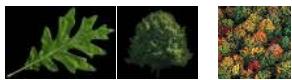
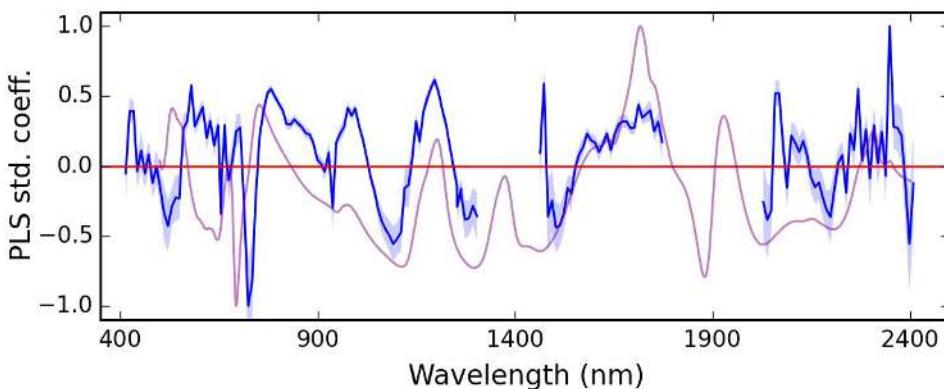
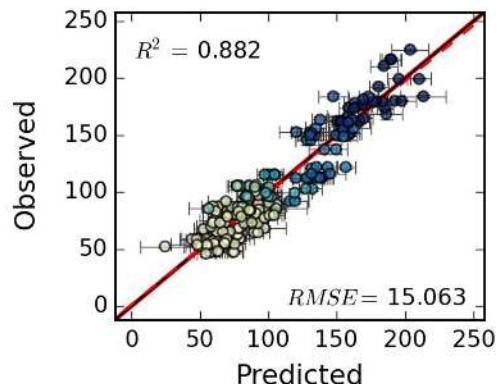
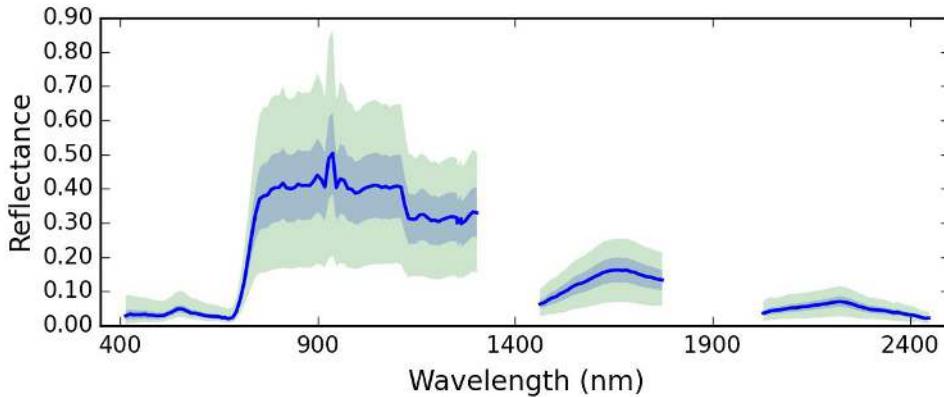
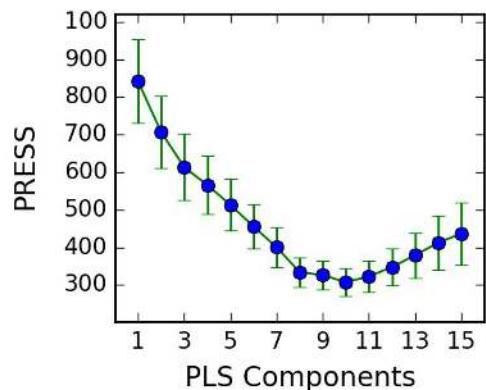


Figure: Adam Chlubas



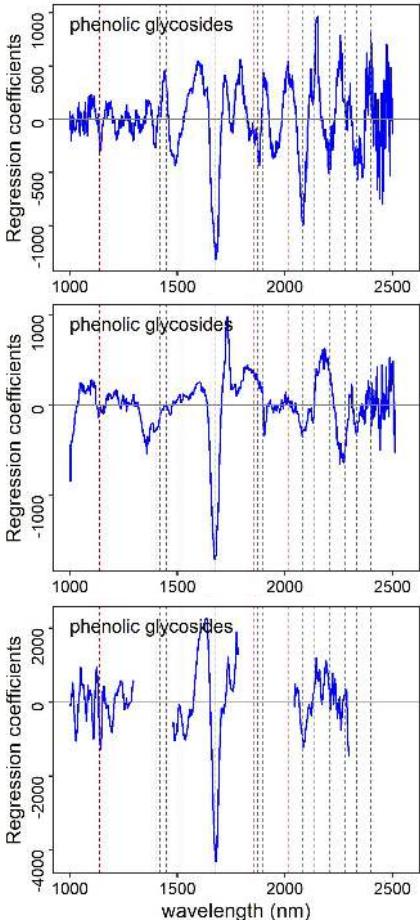
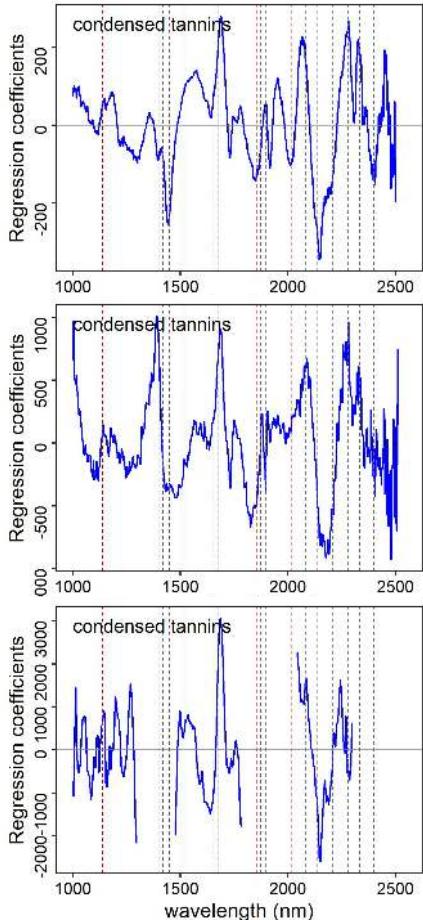
Partial least squares regression

- Chemometric method designed to handle high-dimensional, multicollinear data
- Permutational approach (jackknife) to get model uncertainties



Coefficients

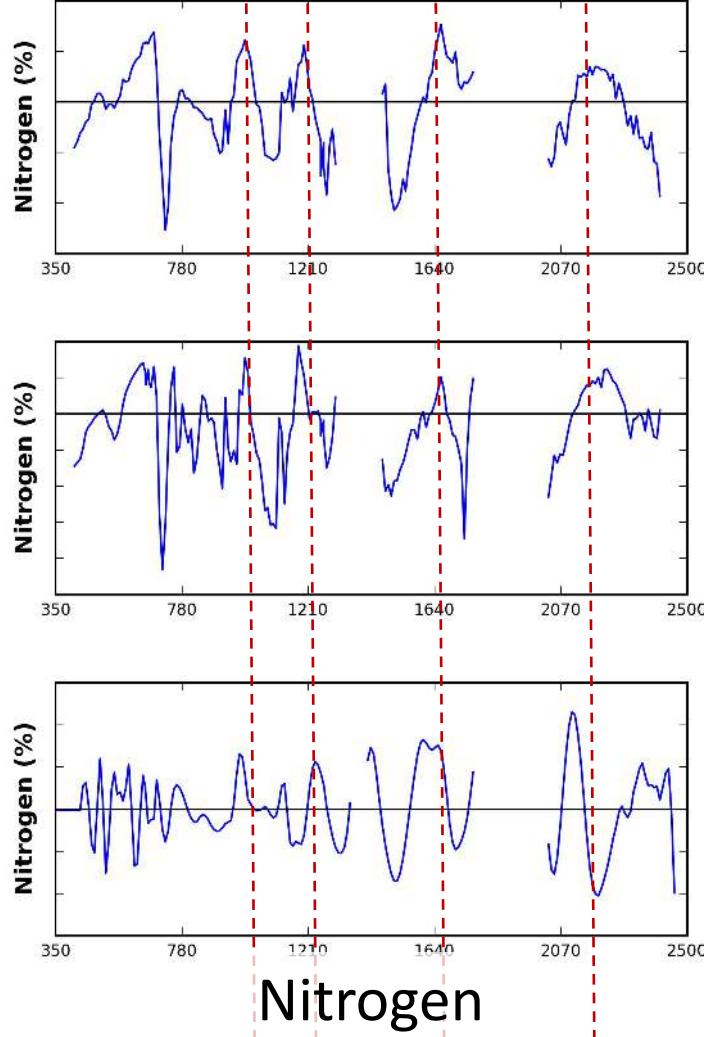
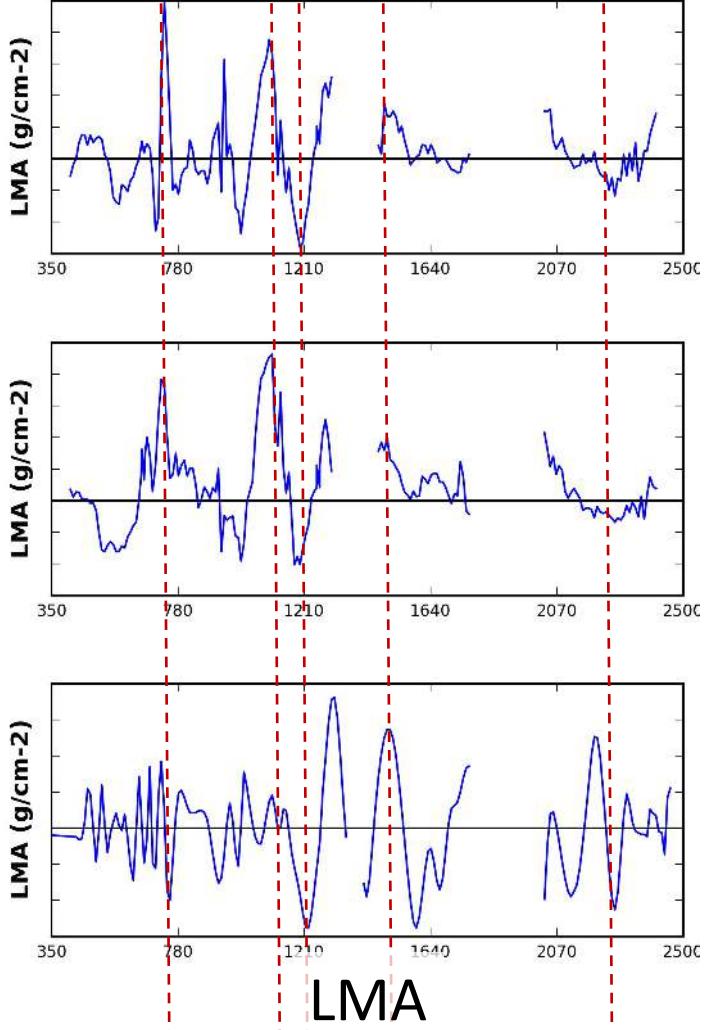
Model comparison



Dry spectra

Fresh spectra

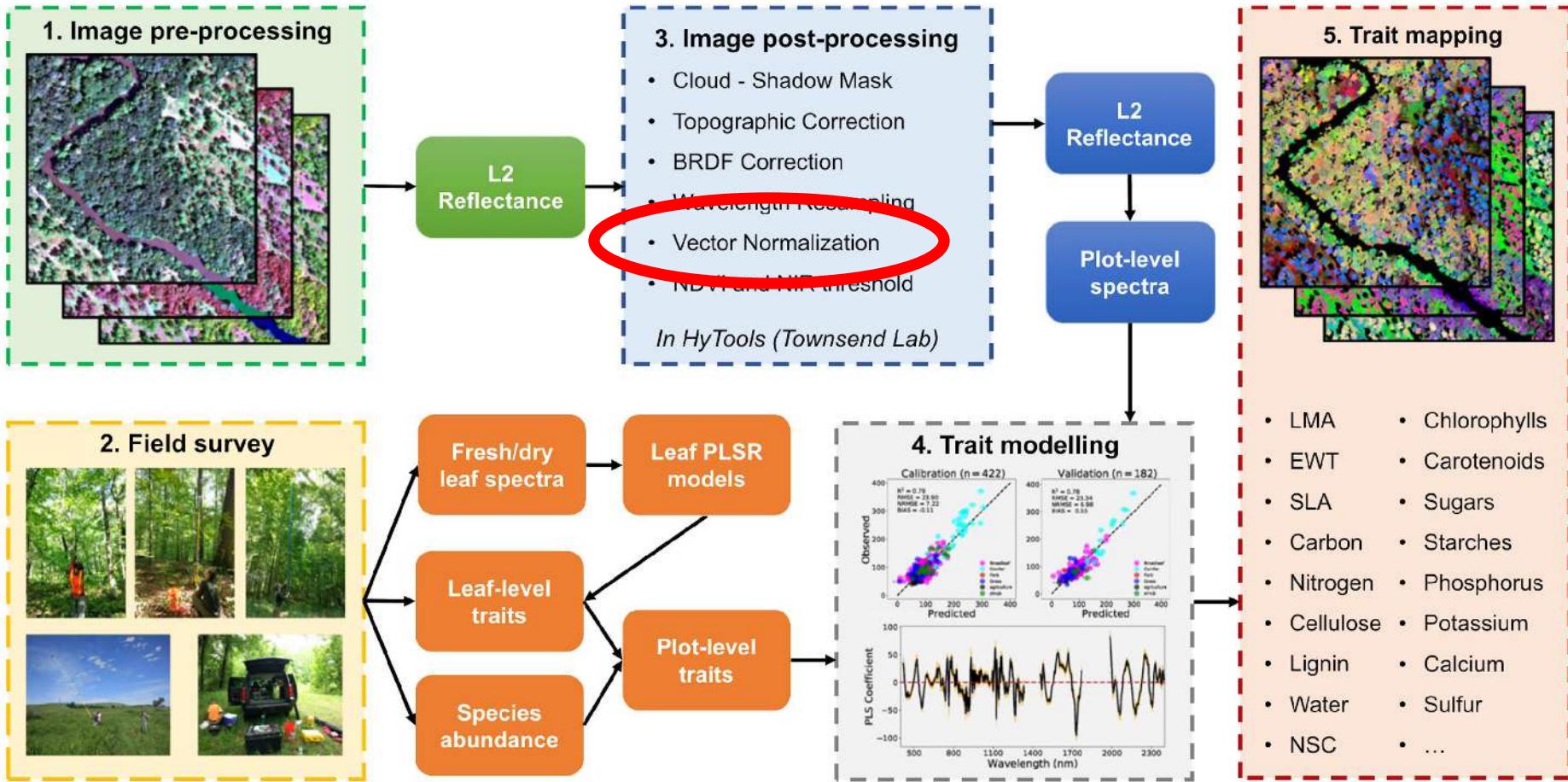
Image spectra



Analyzing your data - normalization

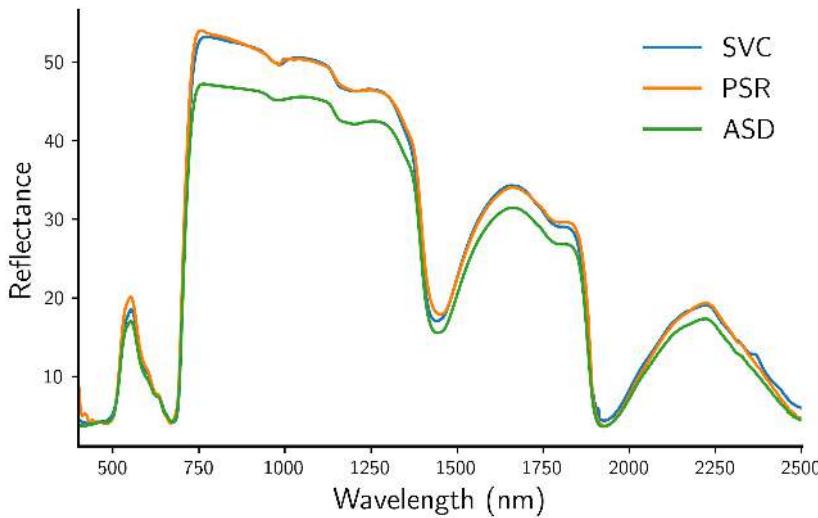
- Many approaches to reduce systematic differences due to differences in lighting
 - Unit-vector normalization
 - Continuum removal

Modeling Overview



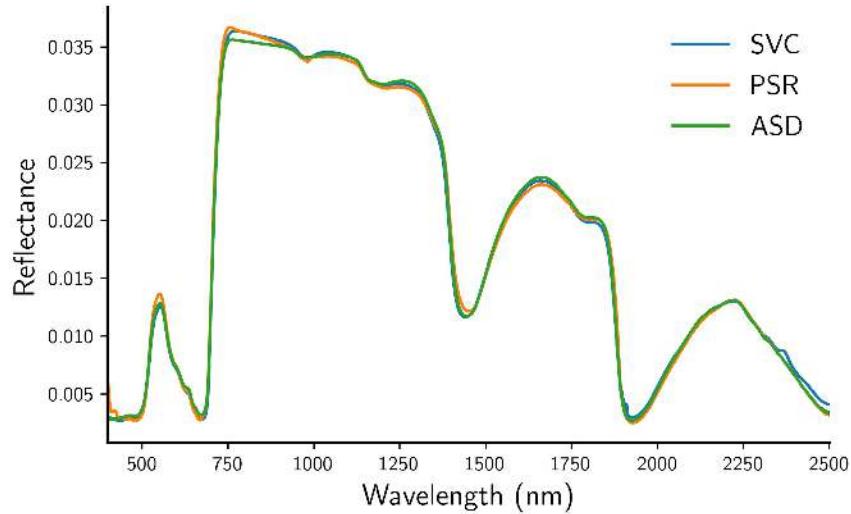
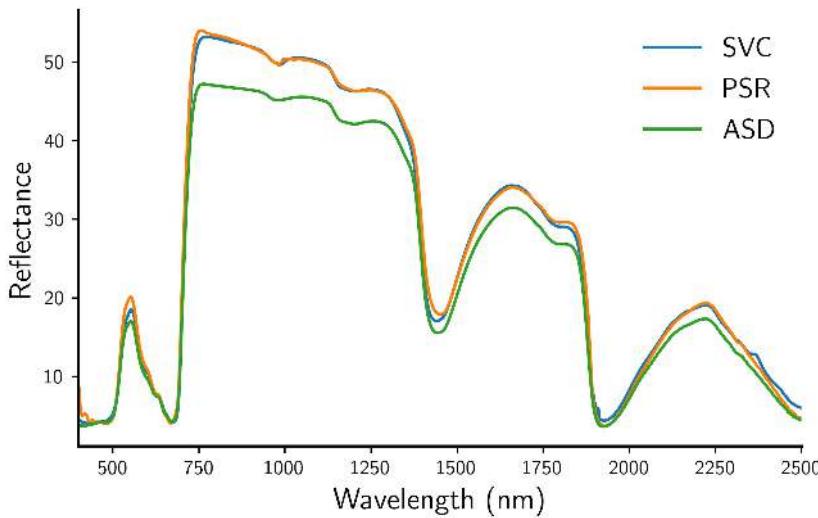
Analyzing your data - normalization

- Many approaches to reduce systematic differences due to differences in lighting
 - Unit-vector normalization
 - Continuum removal



Analyzing your data - normalization

- Many approaches to reduce systematic differences due to differences in lighting
 - Unit-vector normalization
 - Continuum removal



Normalization

- It is a good idea to remove wavelengths you do not plan to use before normalizing

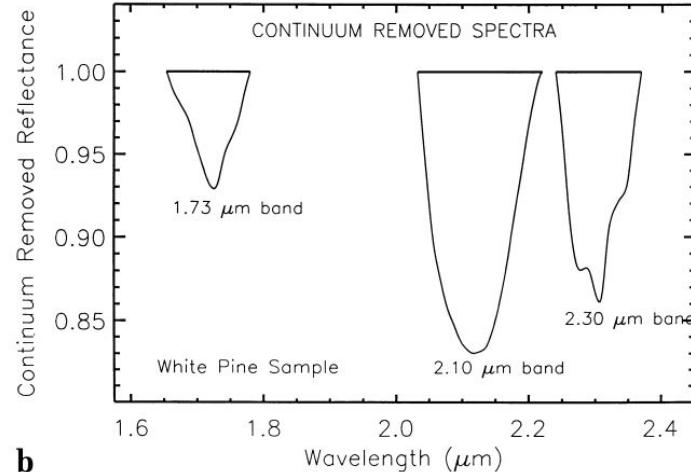
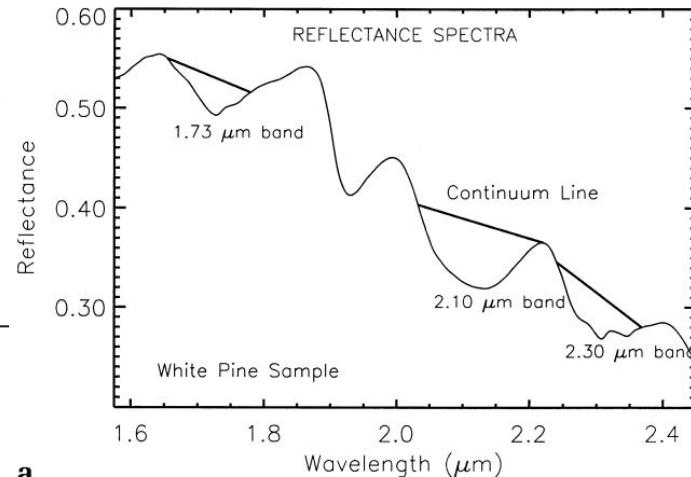
Spectroscopic Determination of Leaf Biochemistry Using Band-Depth Analysis of Absorption Features and Stepwise Multiple Linear Regression

Raymond F. Kokaly* and Roger N. Clark*

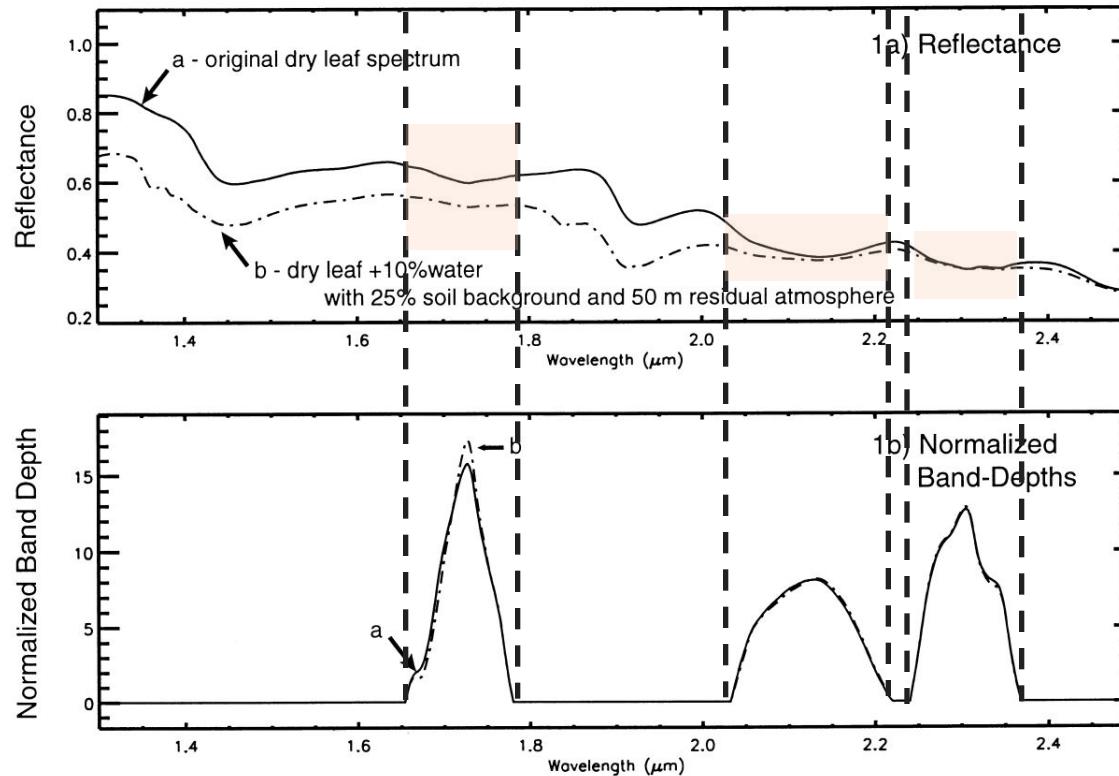
REMOTE SENS. ENVIRON. 67:267–287 (1999)

= continuum removal

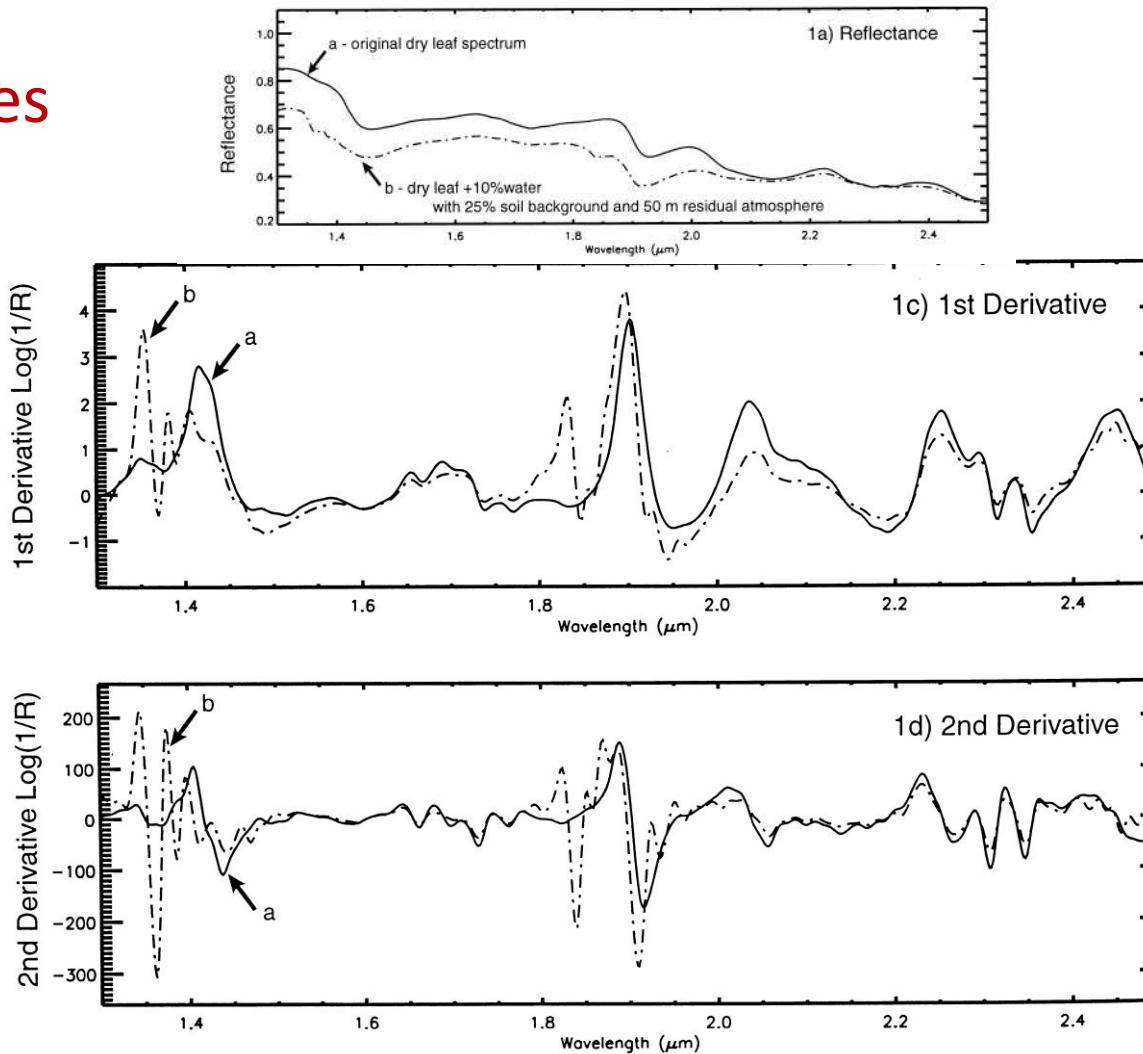
Figure 2. Continuum analysis is demonstrated for a white pine sample. Figure 2a shows the continua used to isolate each major absorption feature in dry leaf reflectance spectrum ($1.73 \mu\text{m}$, $2.10 \mu\text{m}$, and $2.30 \mu\text{m}$). Figure 2b shows the result of continuum removal for the three features. The continua end points are defined in Table 2.



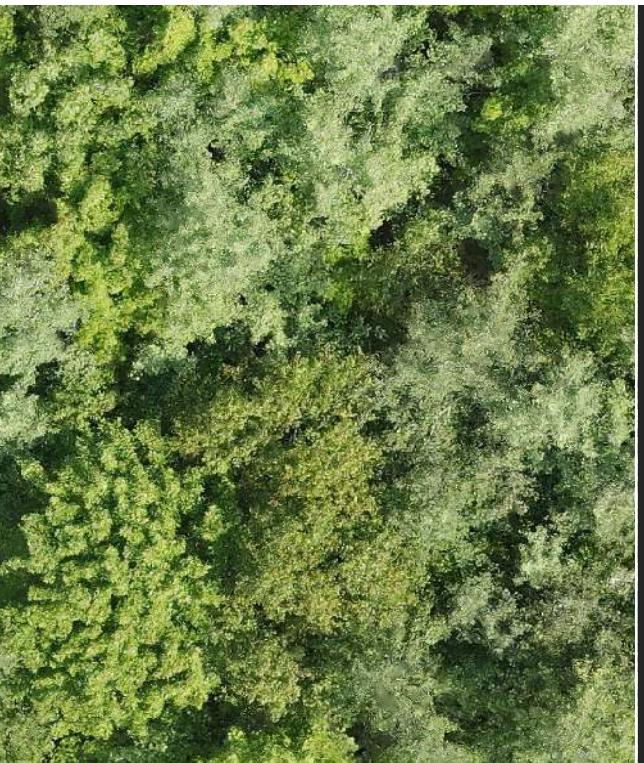
Continuum Removal



Derivatives



Foliar trait modeling with hyperspectral data – an overview



```
htt.WavelengthSelector(wanted_range)
htt.UnitMagnitudeNormalizer()
init_transform = htt.SpectrumDataTransformSequence(
dataset = htt.SpectrumFrameDataset(data_csv=clean_dir/
                                         transform=init_trans

splitter = htt.SpectrumFrameDatasetSplitter(outer_para
                                             calib_inne
                                             deploy_inn
split_data = splitter(sample_ids=dataset.sample_data[])
sample_labels=dataset.sample_data

start_time = time.perf_counter()
oi_n_comps, oi_rmses, oi_r2s, oi_biases = [], [], [], []
oi_mnrmsses, oi_qnrmsses, oi_rnrmsses, oi_snrmsses = [], [], []

for oi in range(n_outer):
    calib_train_transform = htt.SpectrumDataTransformS
    calib_train_dataloader = htt.SpectrumFrameDatasetD

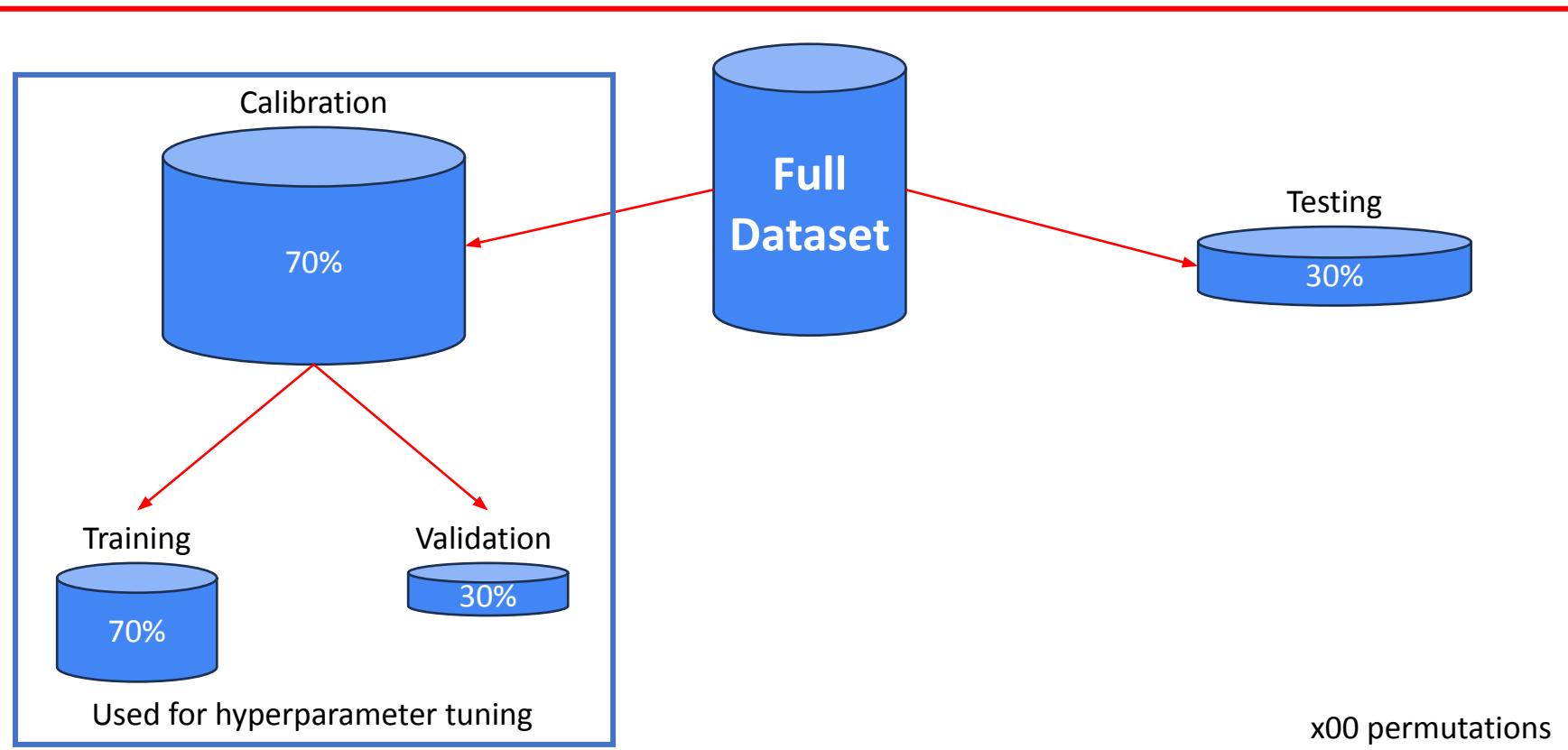
    calib_valid_transform = htt.SpectrumDataTransformS
    calib_valid_dataloader = htt.SpectrumFrameDatasetD

    deploy_train_transform = htt.SpectrumDataTransform
    deploy_train_dataloader = htt.SpectrumFrameDatasetD
```



Split Spectral Data

- Split data into calibration and validation datasets, and also withheld testing set
- Withheld testing set is never used, better if collected separately (such as different year, site, etc.)



Field to table

Fieldwork



2.7
7



1.3
5



0.8
8



Consolidated and curated data

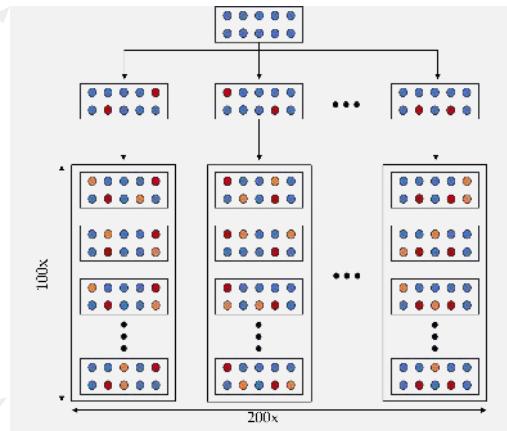
A	B	C	D	E	F	G	H
	0.55033	0.550843	0.550599	0.549292	0.54855	0.548535	2.77
	0.567641	0.568098	0.5683	0.567753	0.565823	0.566529	1.35
	0.62218	0.622497	0.6231	0.621212	0.619791	0.621486	0.88

Table to model (HyTraits)

A	B	C	D	E	F	G	H
0.55033	0.550843	0.550599	0.549292	0.54855	0.548535	2.77	
0.567641	0.568098	0.5683	0.567753	0.565823	0.566529	1.35	
0.62218	0.622497	0.6231	0.621212	0.619791	0.621486	0.88	

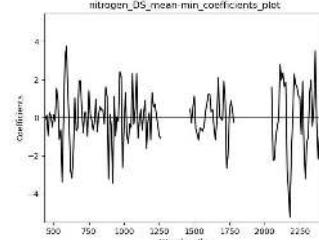
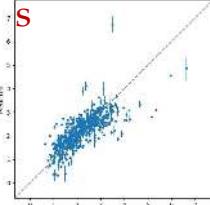
```
import hytraits as H

dataset = H.CSVDataset(spectra_file=<SPECTRA_CSV>,
                      traits_file=<TRAITS_CSV>,
                      trait_column=<TRAIT_NAME>)
splitter = H.CSVDatasetSplitter(split_type='monte_carlo',
                                 n_outers=200,
                                 n_inners=100,
                                 train_valid_test_props=(0.6, 0.2, 0.2))
transform = H.Compose([H.ToDevice(device='cpu'),
                      H.WavelengthsRemoval(remove_ranges=<RANGE>),
                      H.UnitVectorNormalization()])
trainer = H.PLSRegressionTrainer(n_components=<MAX_NUM_COMPONENTS>,
                                  transform=transform)
models = trainer(dataset=dataset,
                  splits=splits)
```

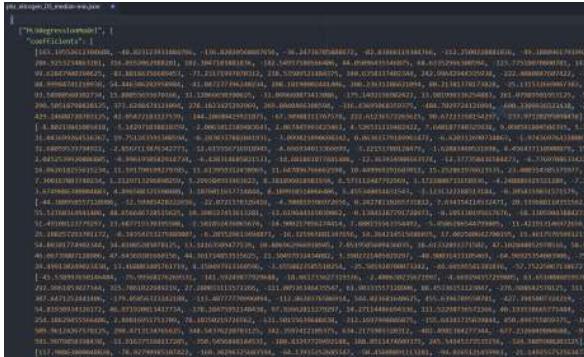


Model JSON file

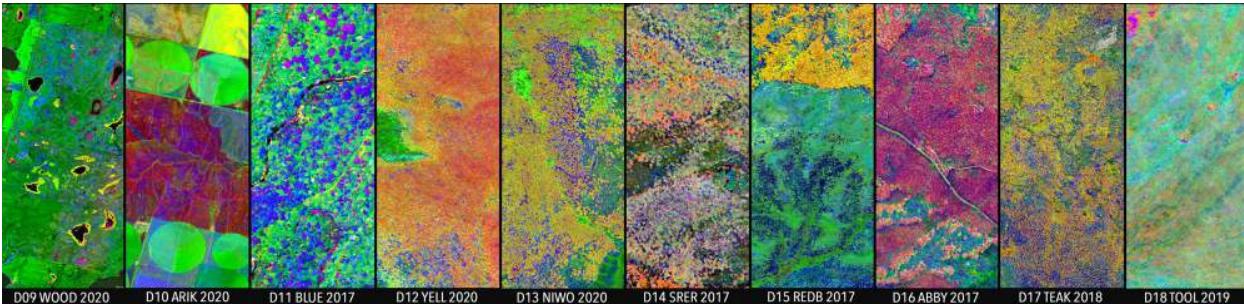
Diagnostic



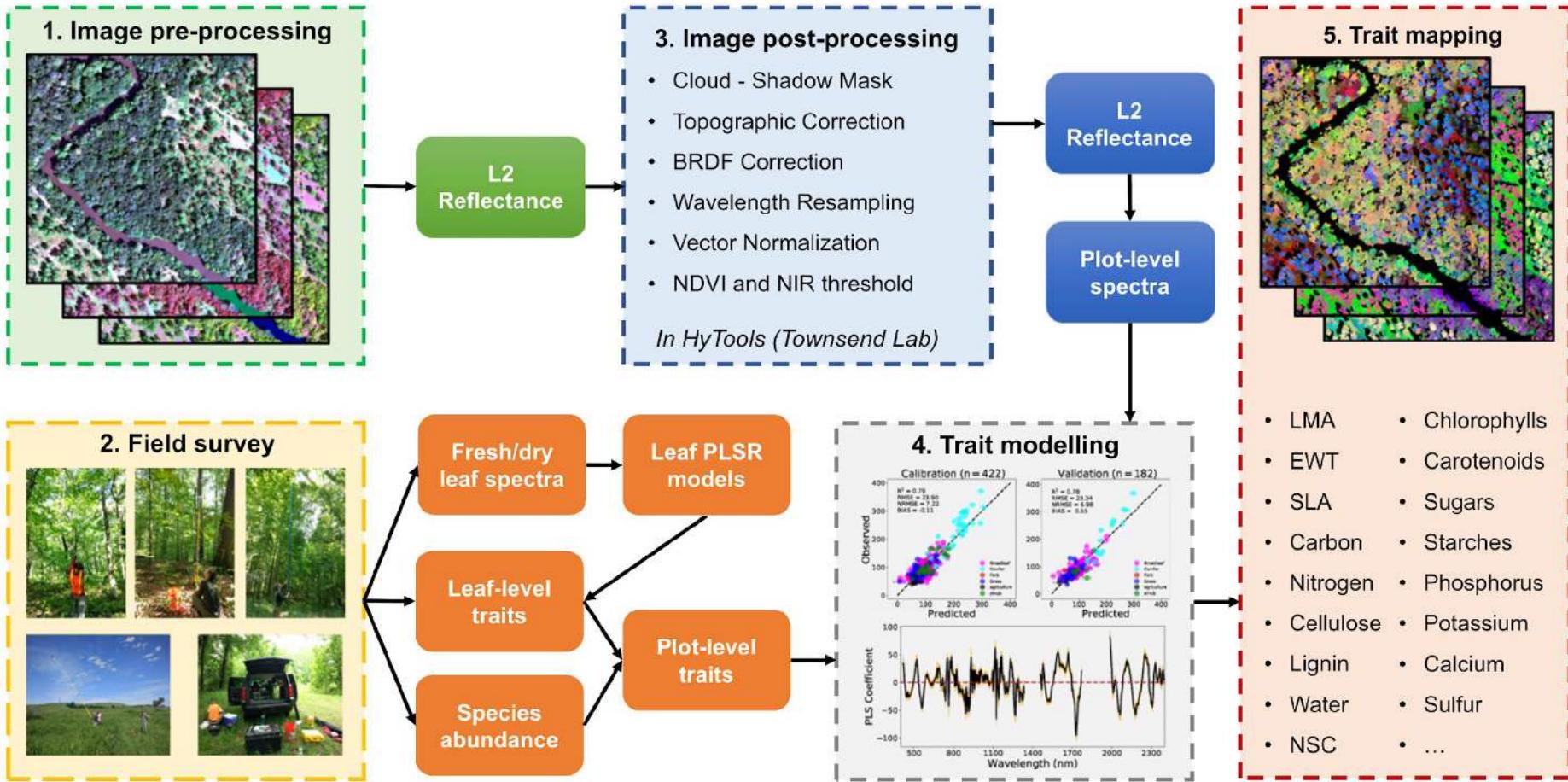
Model to trait maps (HyTools)



HyTools



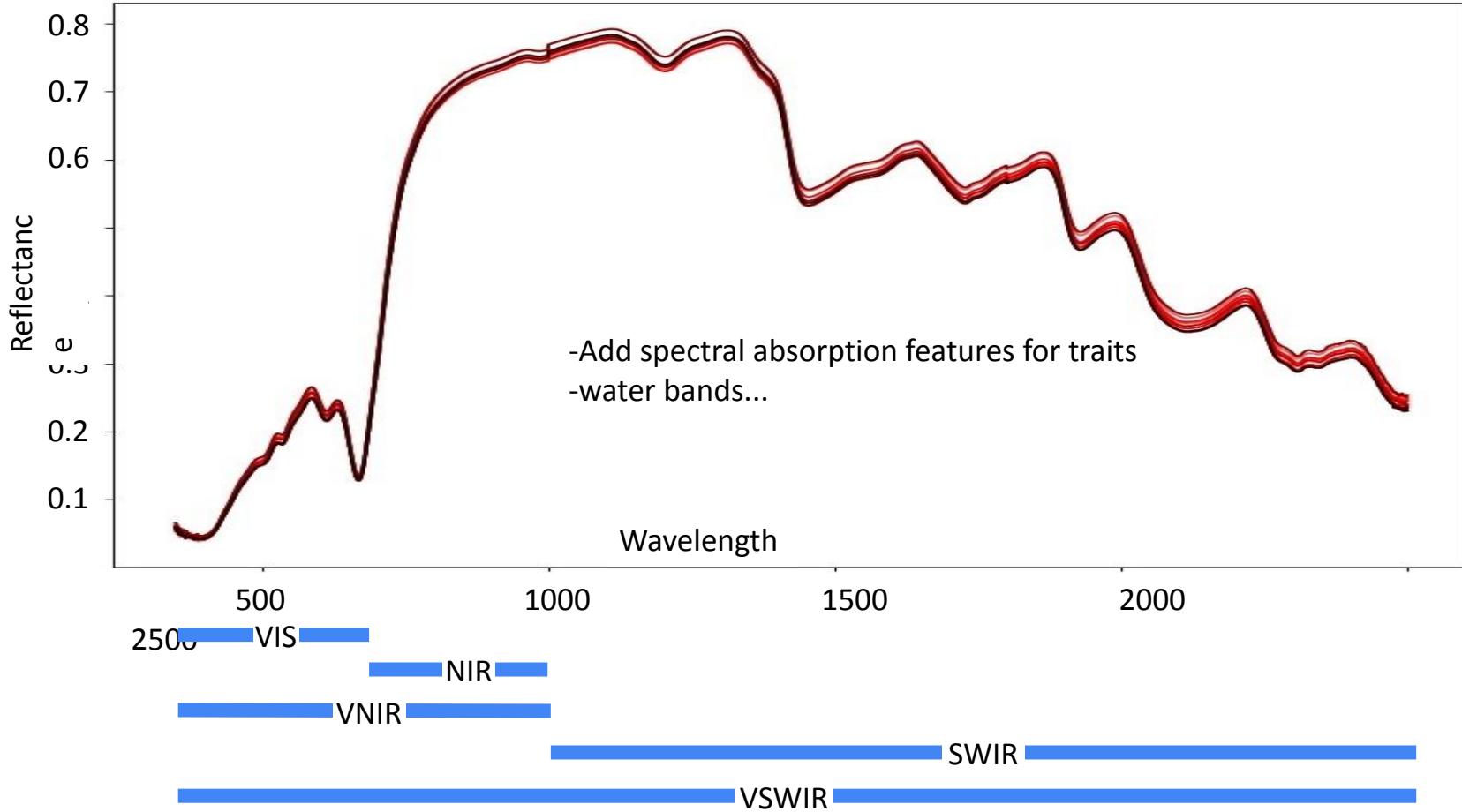
Modeling Overview



PLSR Interpretation

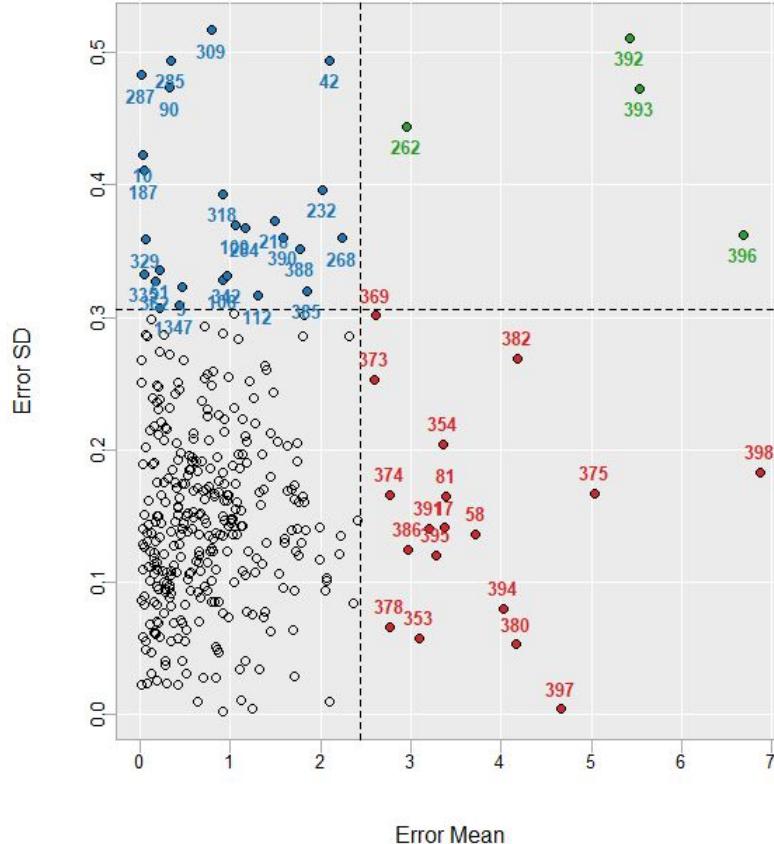
- Coefficients
 - Raw coefficients
 - Standardized coefficients
 - VIP

Model Spectral Range Grouping



Handling Outliers

- Train PLSR model with cross-validation.
- Run PLSR model with a specific number of permutation.
- Use a standard deviation threshold to remove outliers.

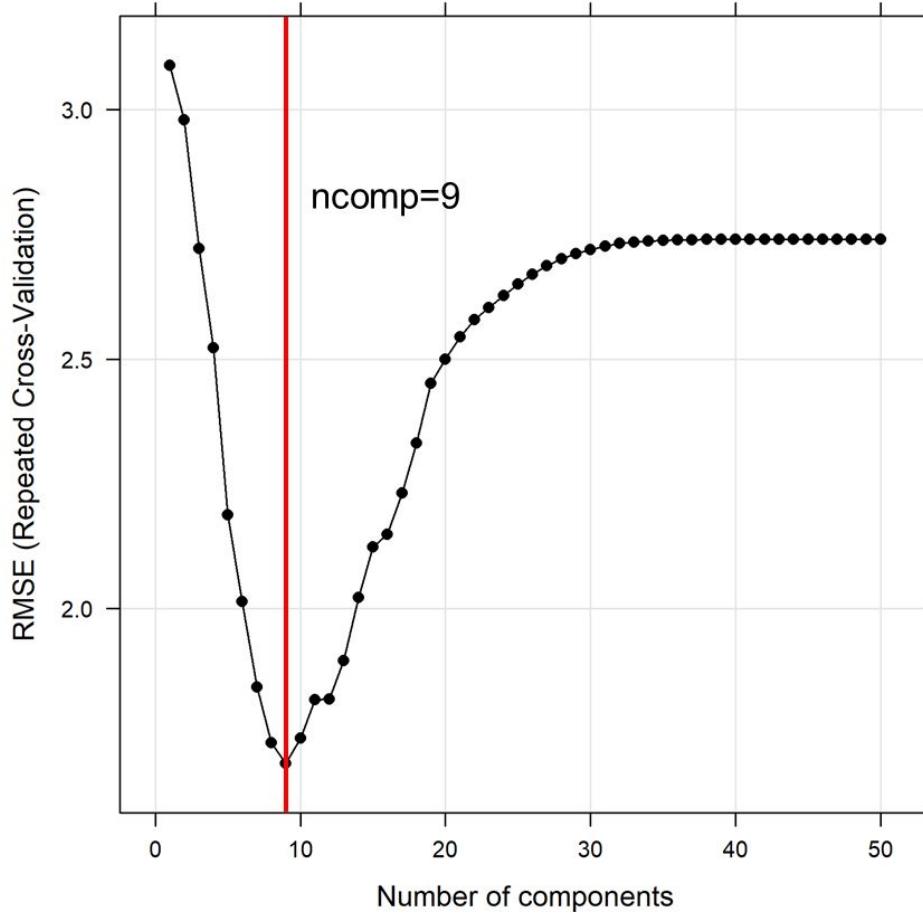


Permutational PLSR

- We quantify uncertainties by running up to 500 models for each trait and using the variation as metric of error

Hyper-parameter Tuning

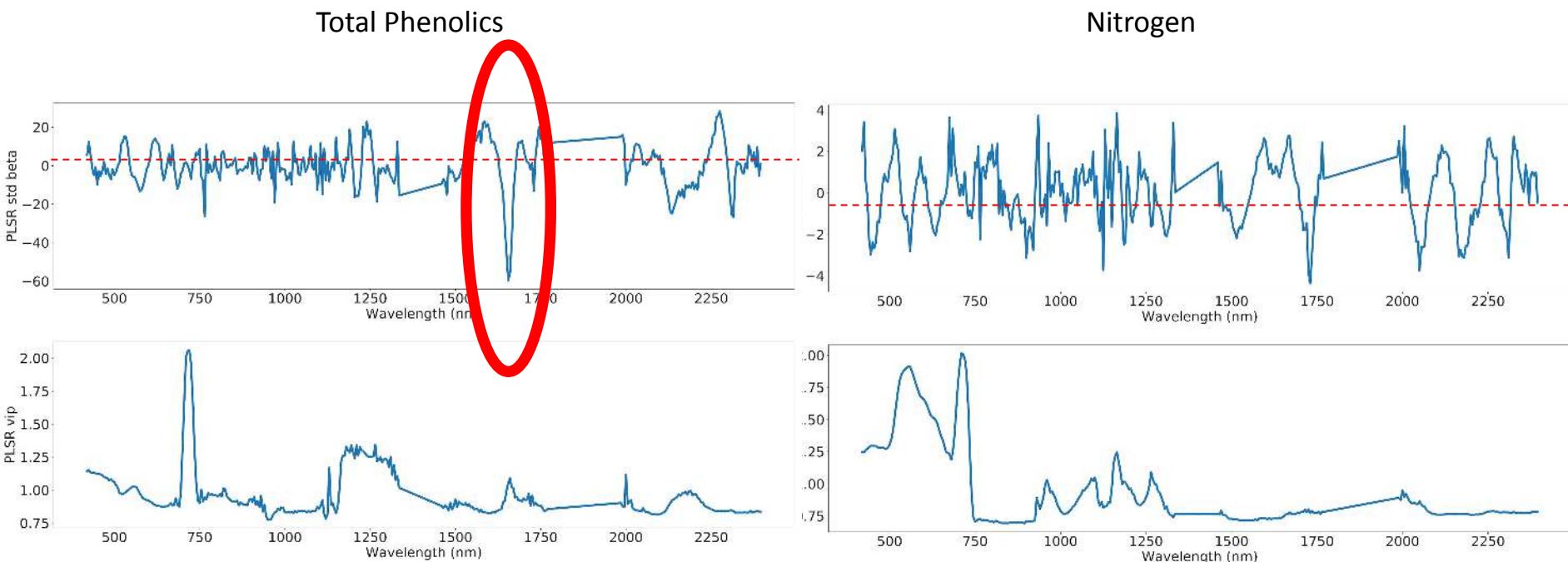
Determine number
of components
(latent vectors)



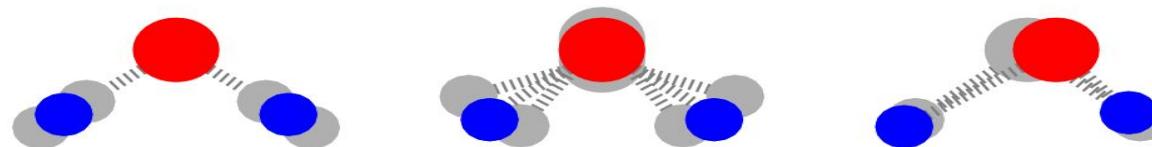
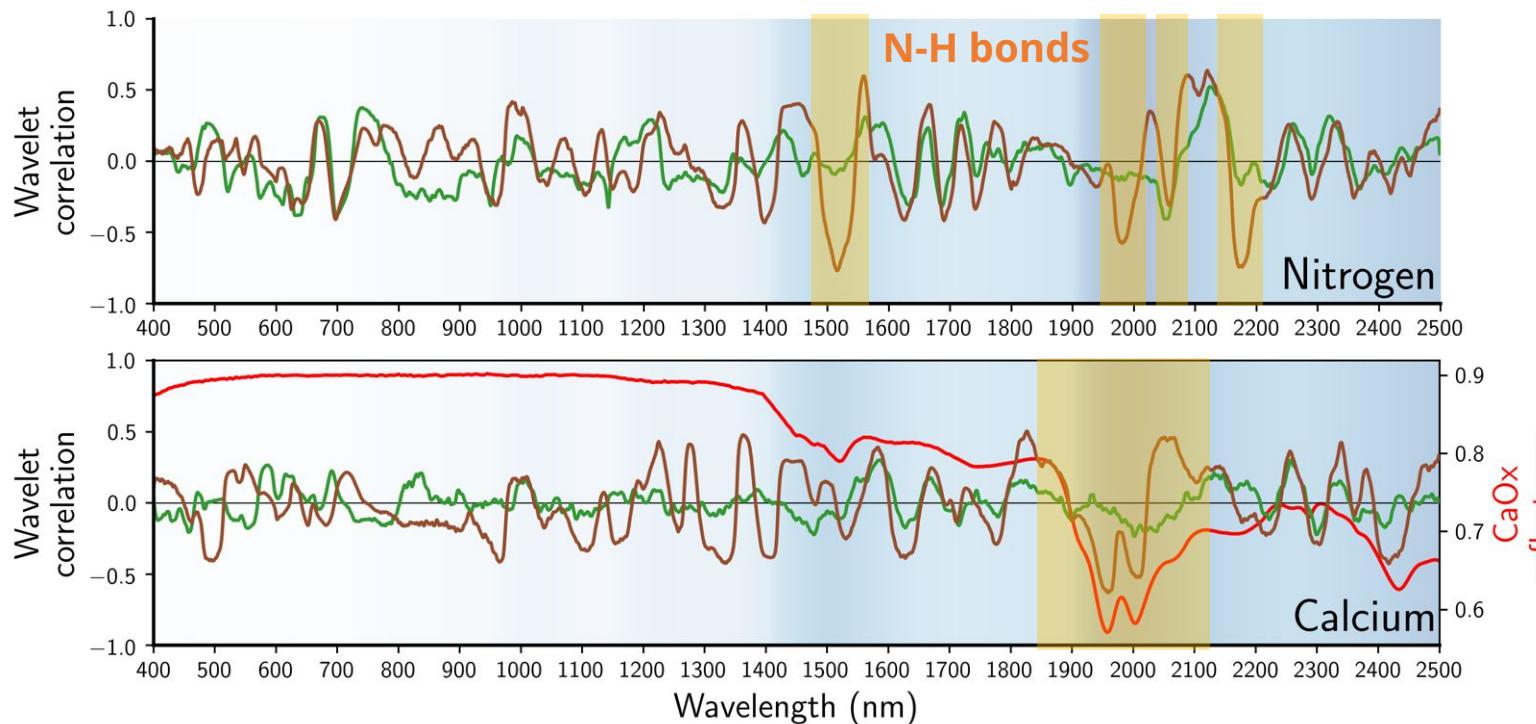
Model Diagnostics

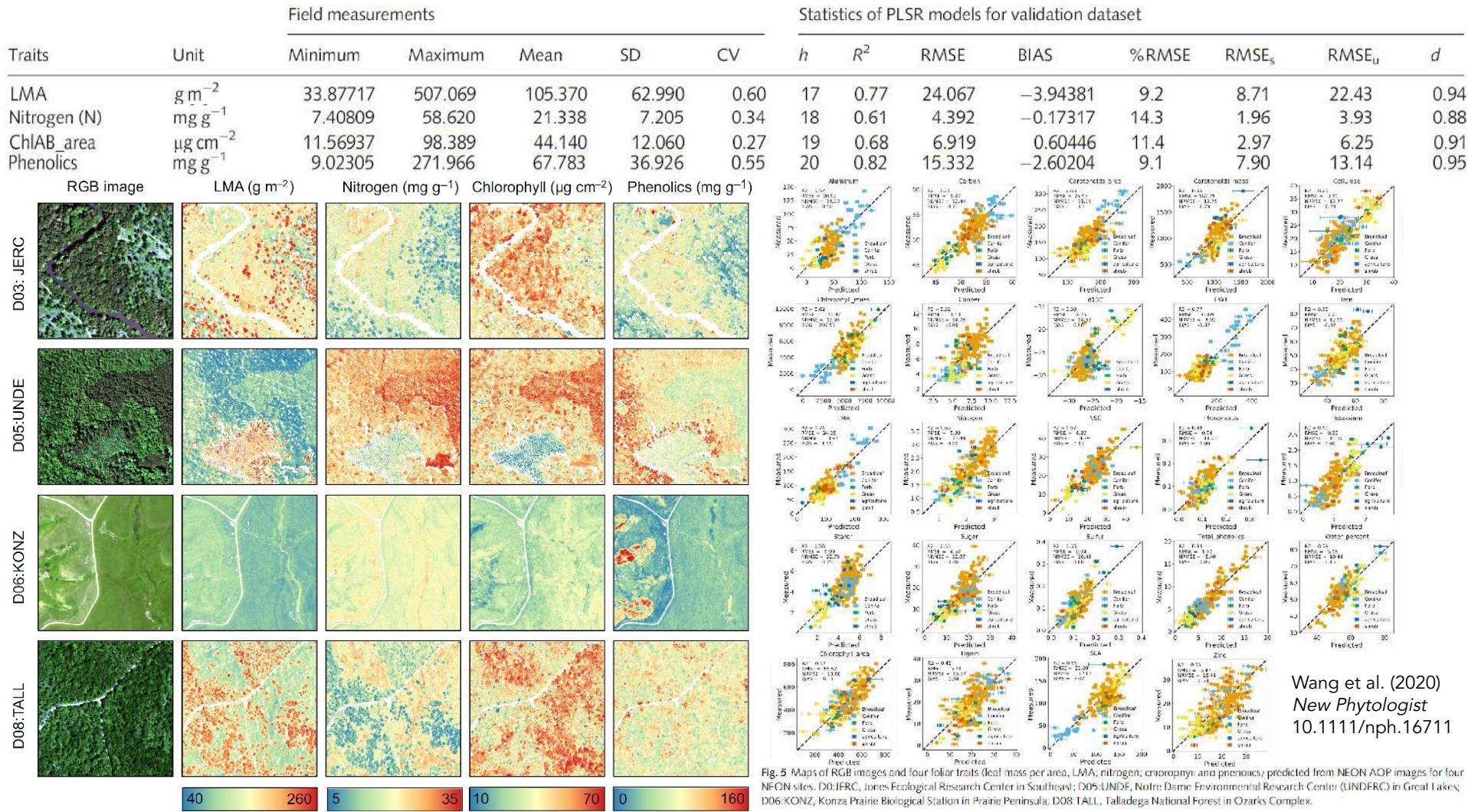
- Diagnostics come from model building, the cross-validation step, and the independent validation step
- R^2
- Root mean squared error
- Normalized root mean squared error (mean, range)

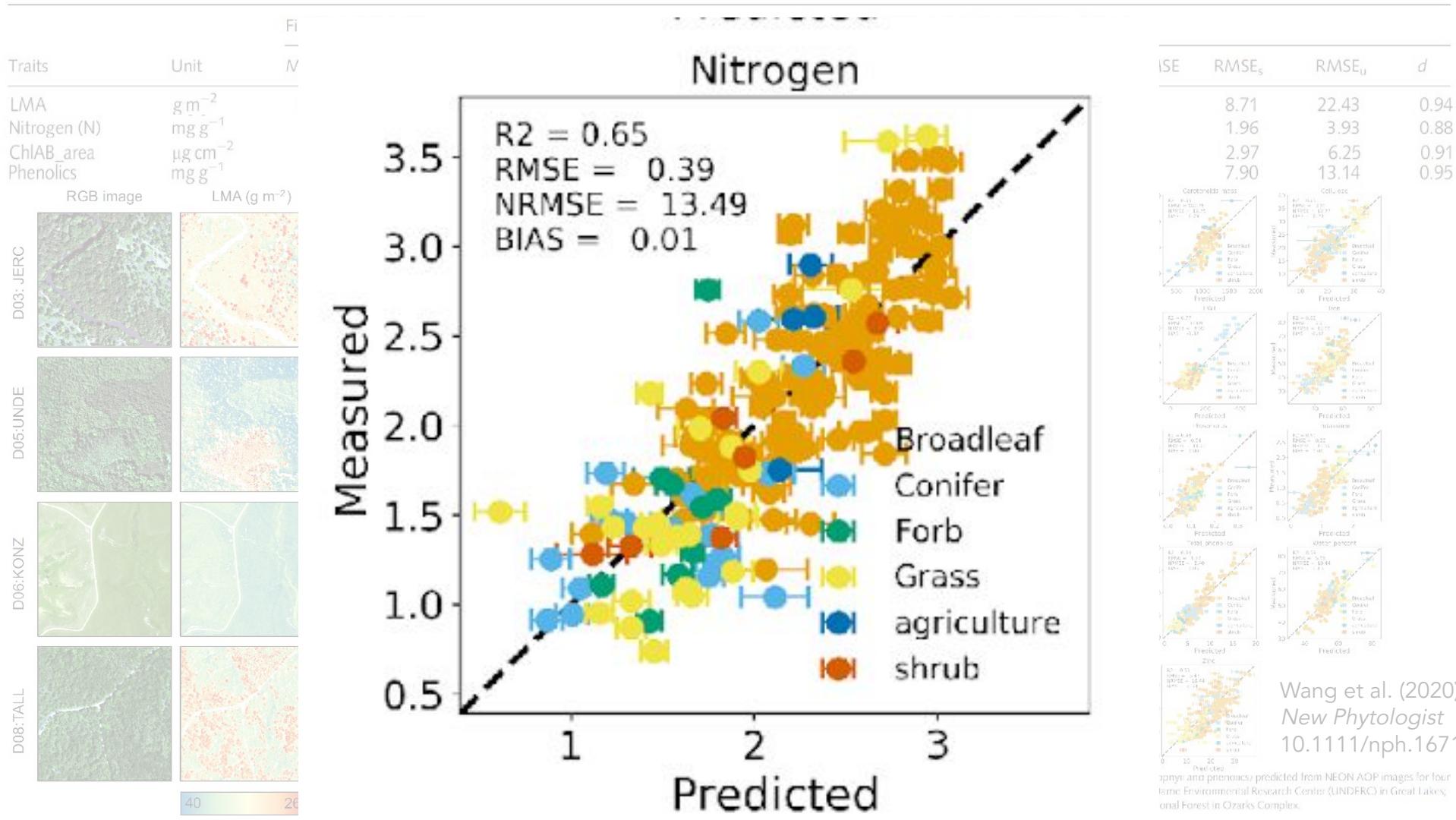
PLS coefficients and model VIPs



Spectra-trait correlations







True Color

Table
Mountain

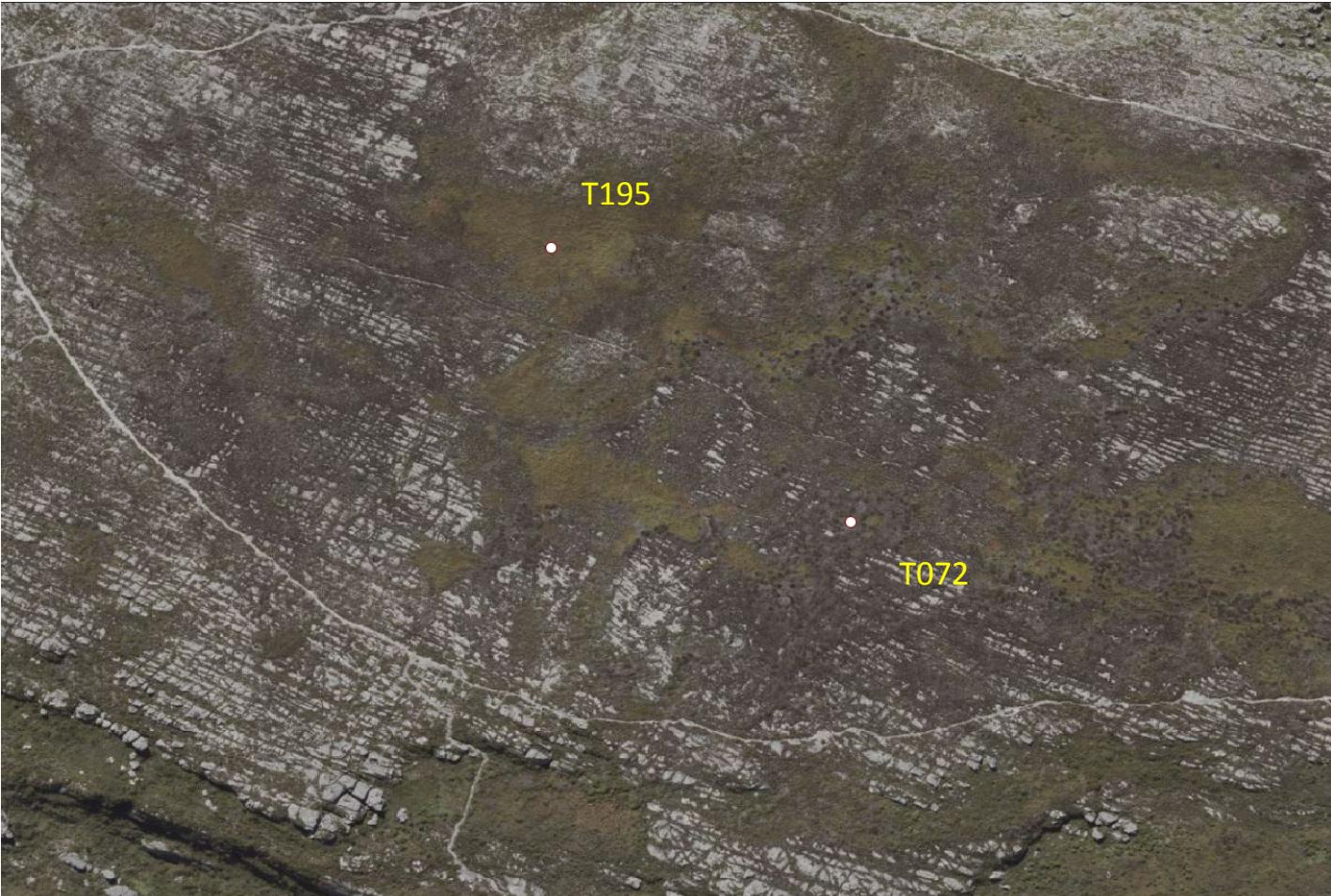


True-color

Close-up of two vegetation plots (white dots), T195 and T072 on top of Table Mountain.

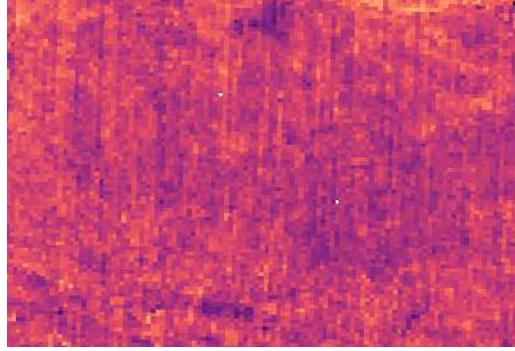
T195 is dominated by Anthochortus (Restionaceae >90% cover).

T072 is a mix of Elegia and Anthochortus, likely lower cover.

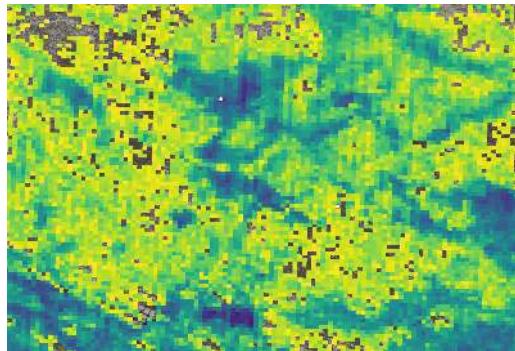


T195 is dominated by Anthochortus
(Restionaceae >90% cover).

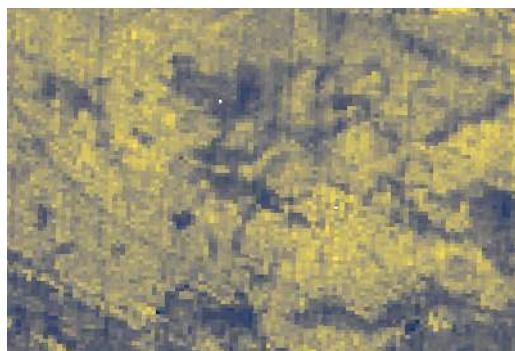
T072 is a mix of Elegia and
Anthochortus, likely lower cover.



Nitrogen

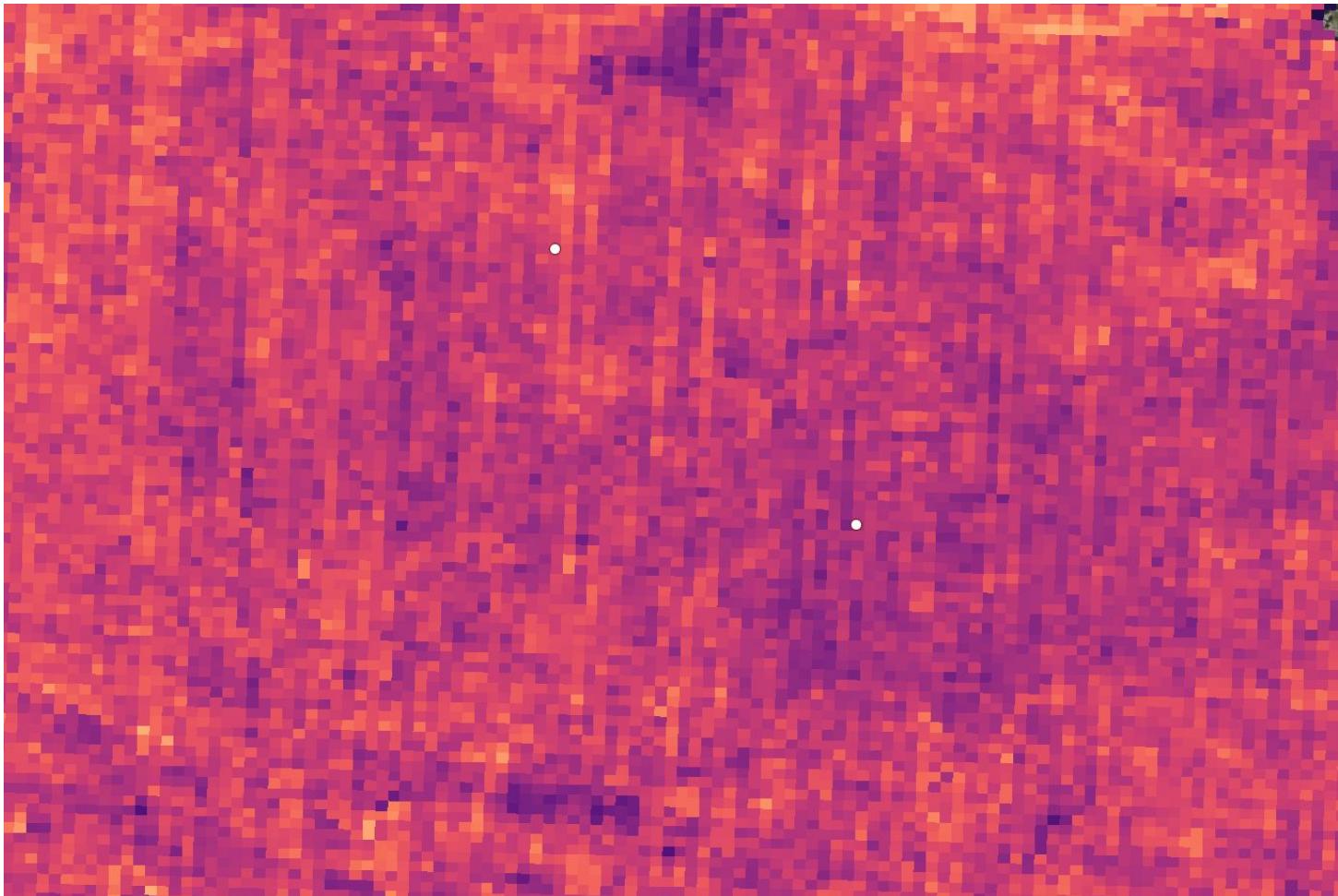


Non-structural
carbohydrates

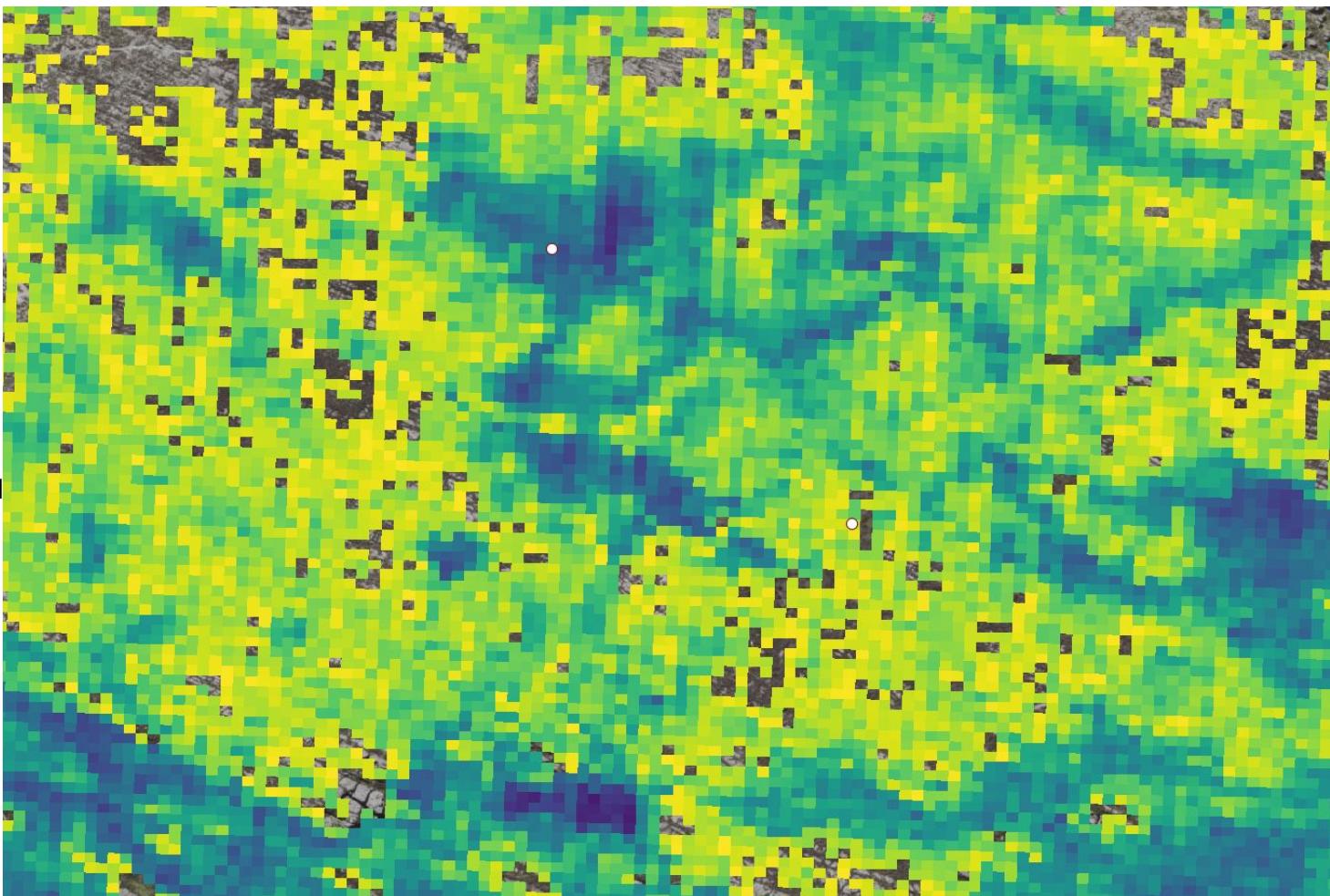


Phenolics

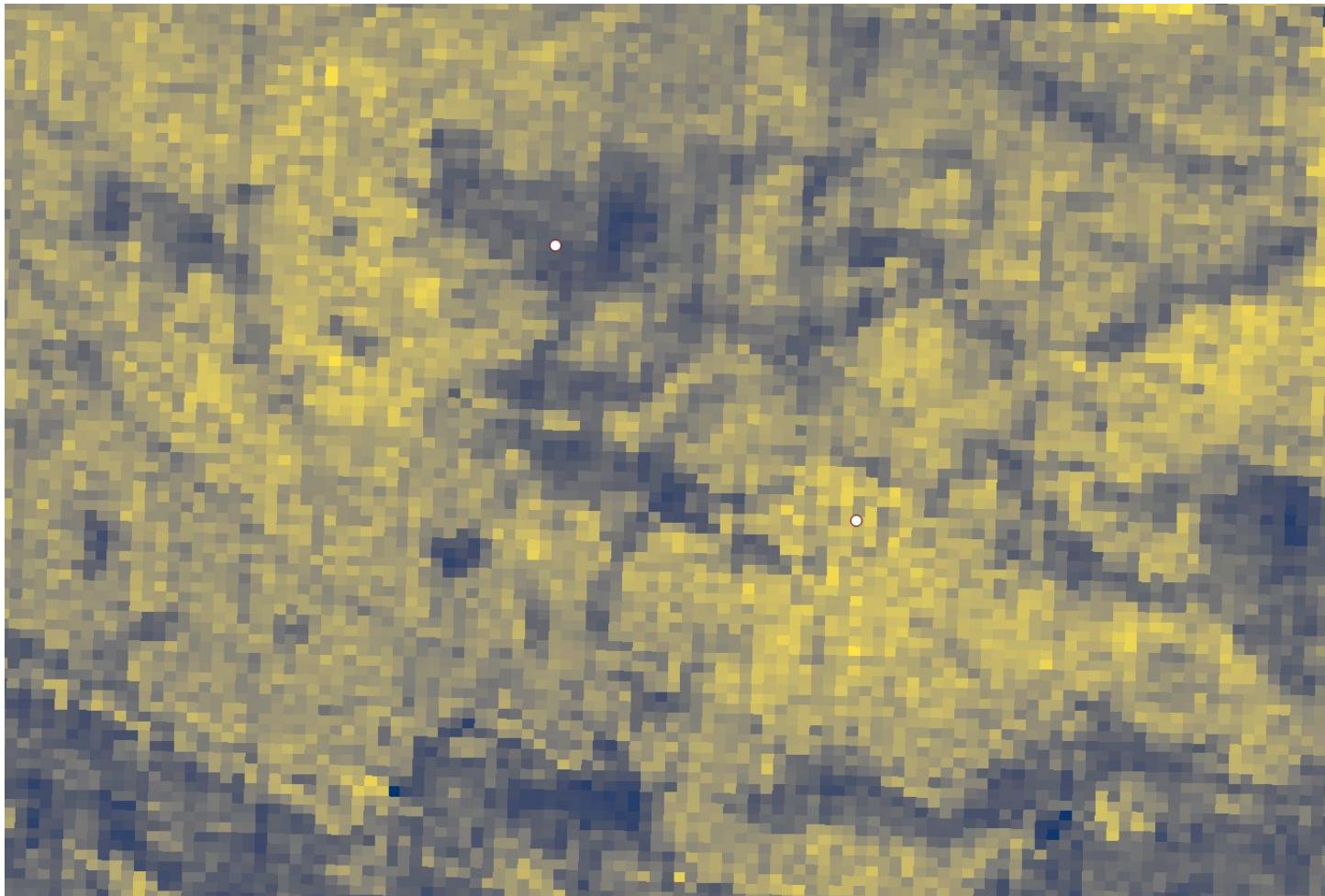
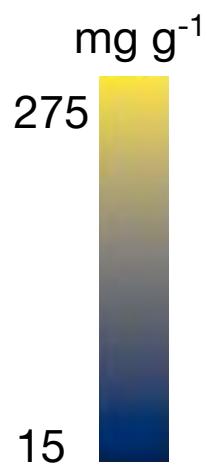
Nitrogen

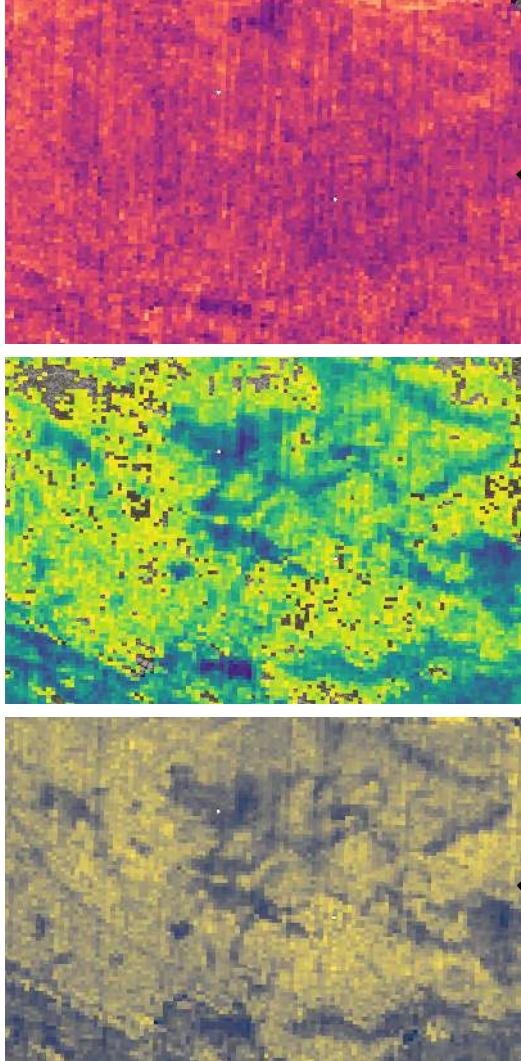


NSCs

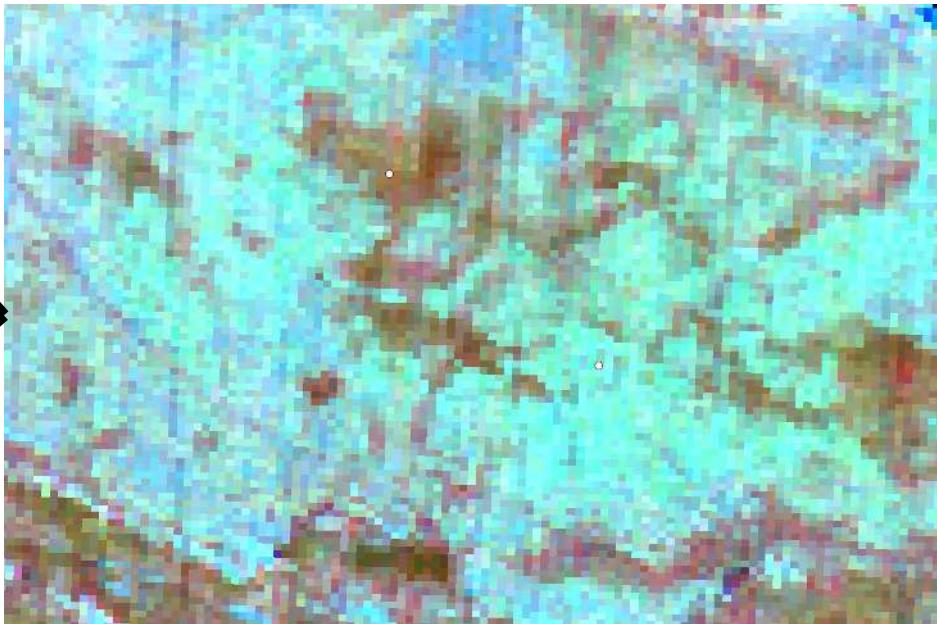


Phenolics





Trait ternary map (Redder pixels = Nitrogen predominates, Greener pixels = Phenolics predominate, bluer pixels = NSCs predominate)



T195 is dominated by Anthochortus (Restionaceae >90% cover).

T072 is a mix of Elegia and Anthochortus, likely lower cover.

True Color

Table
Mountain



Ternary map of
the same traits
as before over
Table Mountain

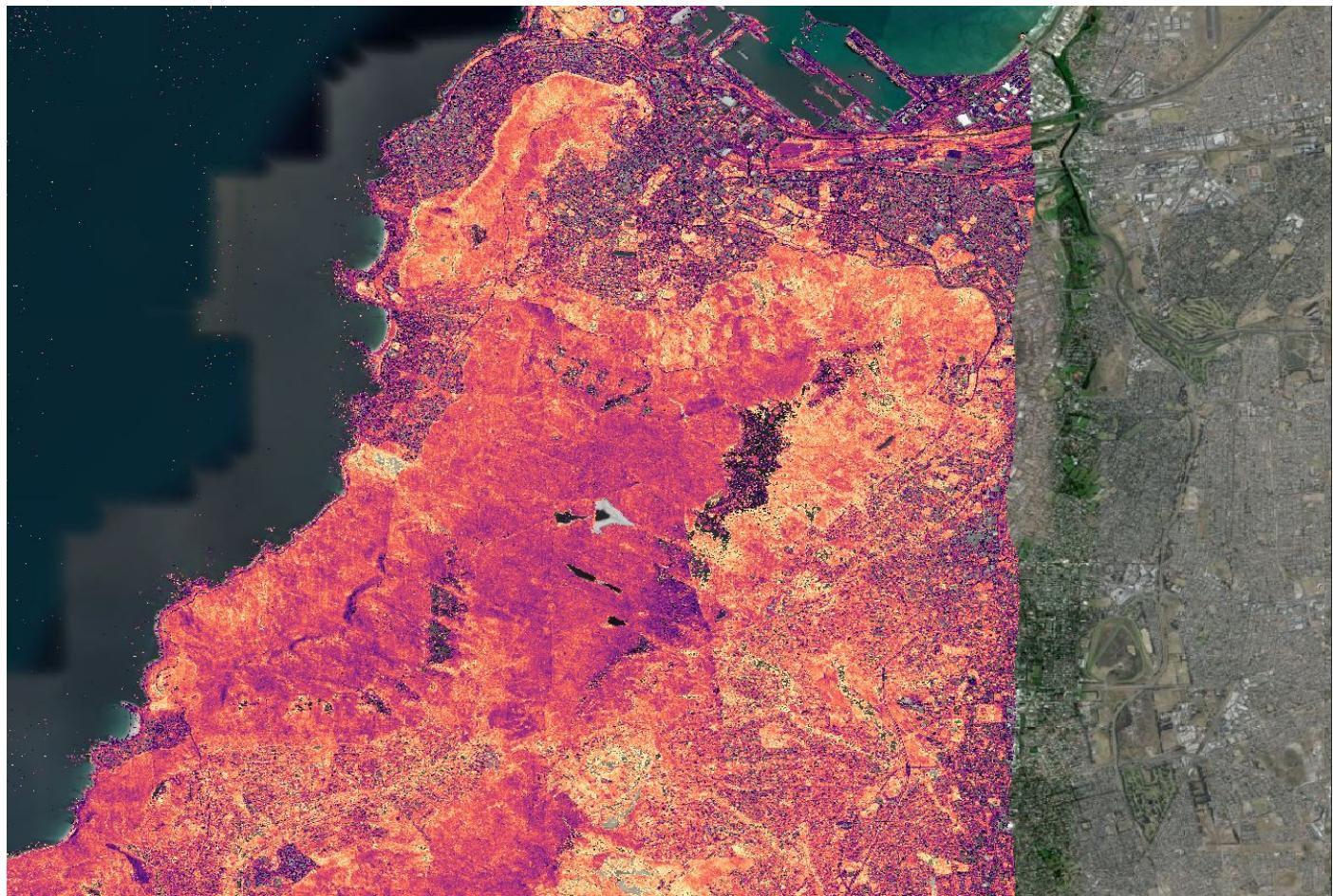
Red = nitrogen

Green = NSCs

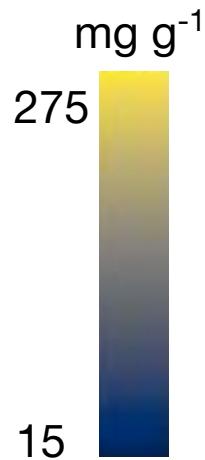
Blue = Phenolics



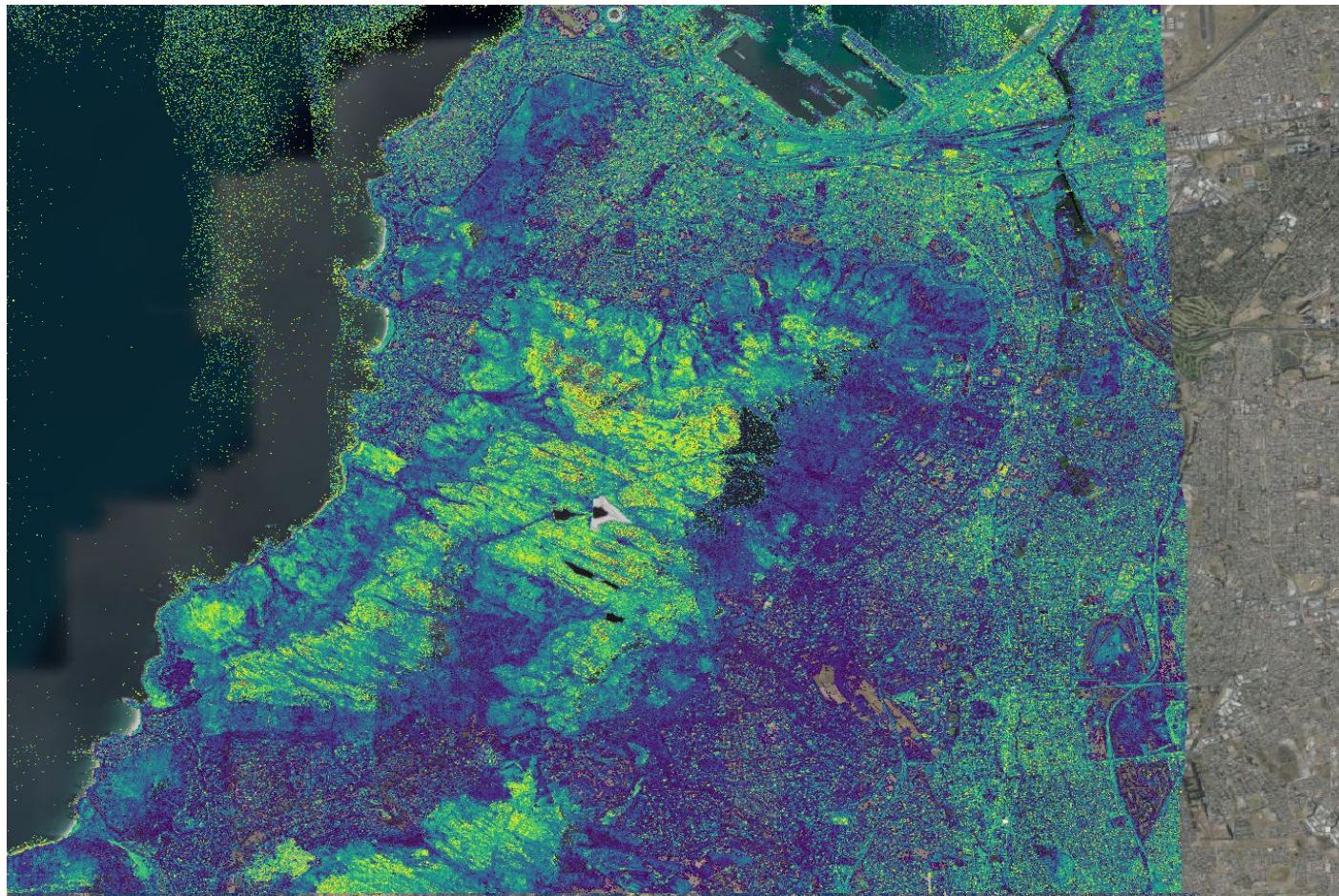
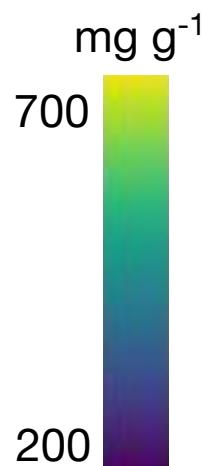
Nitrogen map over Table Mountain



Phenolics map over Table Mountain



NSCs map of Table Mountain



True Color

Cape
Peninsula

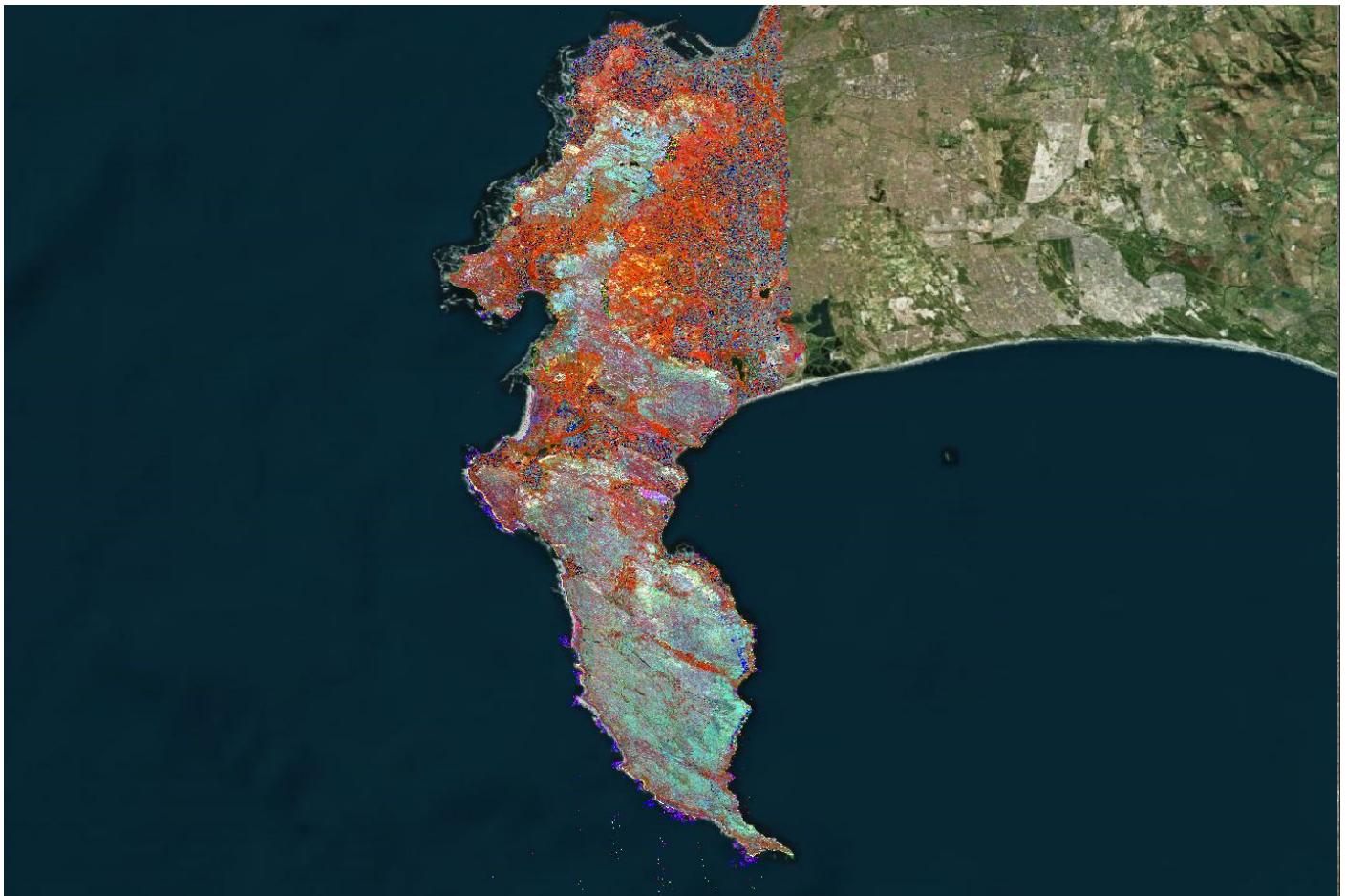


Ternary map of
the Peninsula

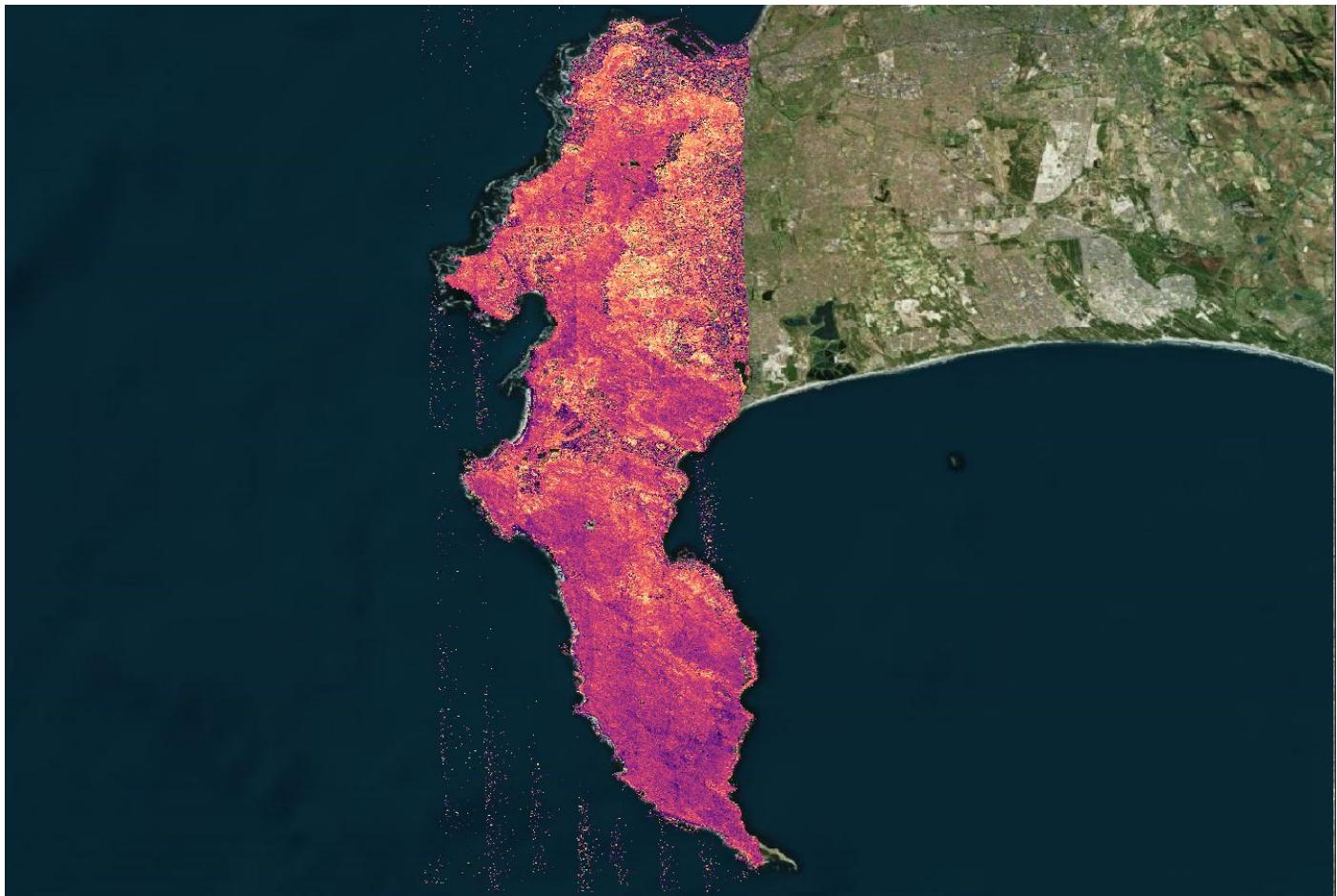
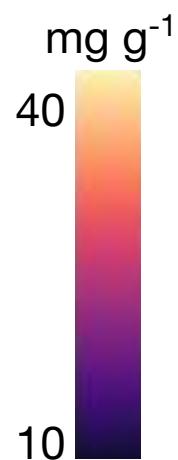
Red = nitrogen

Green = NSCs

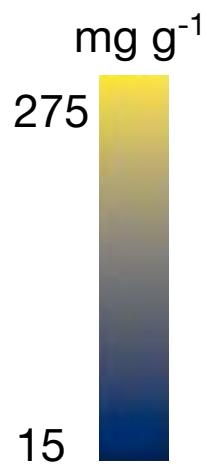
Blue = Phenolics



Nitrogen map of the peninsula



Phenolics map of the peninsula



NSCs map
of the
peninsula

